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OM protein - protein search, using sw model

Run on: June 27, 2002, 16:03:31 ; Search time 73.16 Seconds
(without alignments)
215,589 Million cell updates/sec

Title: US-09-781-077-2

Perfect score: 760

Sequence: 1 MARYMLLLAVVLTGELW.....GLSSCKCKGCKSKBSISL 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11107396 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_032802.*

- 1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	760	100.0	142	22 AAG78114	Human insulin homo
2	148	19.5	135	21 AAY95771	Mouse insulin fami
3	147	19.3	135	19 AAW37926	Mouse zins3 protei
4	126.5	16.6	135	19 AAW37925	Human zins3 protei
5	126.5	16.6	135	20 AAY01961	Pro-insulin-like p
6	126.5	16.6	135	21 AAB00173	PRO182 polypeptide
7	126.5	16.6	135	21 AAB24391	Human PRO182 prote
8	126.5	16.6	135	21 AAY95770	Human insulin fami
9	126.5	16.6	135	21 AAB3228	PRO182 Polypeptide
10	126.5	16.6	135	22 AAM24033	Human EST encoded
11	126.5	16.6	135	22 AAU12309	Human PRO182 polyp

12	126.5	16.6	135	22 AAB20110	Human immunostimul
13	126.5	16.6	135	22 AAB53072	Human angiogenesis
14	111.5	14.7	185	5 AAP40108	Sequence of human
15	109.5	14.4	185	5 AAP40156	Amino acid sequenc
16	108.5	14.3	182	5 AAP40156	Sequence of porcine
17	107.5	14.1	162	11 AAR07987	H2 prorelaxin gene
18	106.5	14.0	182	4 AAP30392	Sequence of porcine
19	102.5	13.5	164	11 AAR07988	H2 prorelaxin dedu
20	98.5	13.0	185	5 AAP40154	Sequence of human
21	96.5	13.0	185	5 AAP40155	Sequence of human
22	94.5	12.4	185	5 AAP40155	Amino acid sequenc
23	92.5	12.2	40	17 AAP96006	Asymmetry sequence
24	92	12.1	30	20 AAY01963	Insulin-like pepti
25	92	12.1	31	21 AAY95773	Human zins3 B chal
26	89.5	11.8	150	16 AAR64904	Prorelaxin fragme
27	88.5	11.6	134	21 AAY71544	Drosophila melanog
28	88.5	11.6	134	21 AAY99807	Drosophila dmsl i
29	88.5	11.6	134	22 ABB62638	Drosophila melanog
30	88.5	11.6	188	19 AAW47547	Rat zins2 testis-s
31	87	11.4	220	22 AAU02911	Angiotensin conver
32	86.5	11.4	110	22 AAB84818	Protein. Unidenti
33	86.5	11.4	178	14 AAR31958	Squamous cell spec
34	84.5	11.1	110	2 AAP10042	Sequence encoded b
35	84.5	11.1	110	2 AAP10053	Sequence of prepro
36	84.5	11.1	110	5 AAP40309	Human preproinsuli
37	84.5	11.1	110	20 AAY06608	Human preproinsuli
38	84.5	11.1	110	21 AAB26765	Human insulin. Ho
39	84.5	11.1	110	21 AAB06144	Human Insulin used
40	84.5	11.1	110	21 AAY70366	Human proinsulin
41	84.5	11.1	110	21 AAY44367	Human proinsulin
42	84.5	11.1	110	22 AAG65877	Human pre-proinsul
43	84.5	11.1	110	22 ABE10337	Secretory cell lin
44	84.5	11.1	110	22 AAB35424	Human insulin prec
45	82.5	10.9	110	22 AAB48847	

ALIGNMENTS

RESULT 1

AAG78114

ID AAG78114 standard; Protein; 142 AA.

XX AAG78114;

DT 21-NOV-2001 (first entry)

DE XX

XX Human insulin homologue polypeptide zins4.

XX Human; insulin; zins4; relaxin; chromosome 19p13.11; cytostatic;

KW antifertility; vasotropic; reproductive disorder; prostate disorder;

KW heart disorder; kidney disorder; gonadal development; pregnancy;

KW pubertal change; menopause; ovarian cancer; testicular cancer; ovulation;

KW polycystic ovarian syndrome; contractile tissue; cardiovascular disease;

KW birth control; impotence; myocyte; endothelial cell; osteoblast;

KW blood pressure; muscle tension; osmotic balance; gene therapy.

OS Homo sapiens.

XX XX

Key Location/Qualifiers

Peptide 1..25

Protein /label= signal_peptide

26..142

/label= mature_protein

26..52

/note= "zins4, Claimed in claim 4"

Region /label= B_chain

34..47

/note= "Claimed in claim 1"

Region /label= B_chain_consensus_sequence_region

37..41

/note= "Given in SEQ ID NO 3"

Region /label= B_chain_conserved_motif

Fri Jun 28 11:32:00 2002

QY 1 MARYMLLLAVVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGSRWRSDILAH 60
 Db 1 marymlllllavvltgelpgaaaraapvgvrlcgrefiravifftcgswrrsdilah 60
 QY 61 EAMGTFPDADADESLAGELDEAMSGSEWLATKSPQAFYRGPRPSWOGTGVLRGSRDV 120
 Db 61 eamgtdfpdadadedslageldeamsgswwlaltkspqafyrgprpswogtgvlrgrsdv 120
 QY 121 LAGLSSSCCKWGCSEISSIC 142
 Db 121 laglssscckwgcskseissic 142

RESULT 2
 AAY95771
 ID AAY95771 standard; Protein; 135 AA.

XX AAY95771;
 XX 07-NOV-2000 (first entry)
 XX Mouse insulin family homologue zins3.
 DE zins3; insulin; relaxin; mouse; NIDDM;
 KW non-insulin dependent diabetes mellitus; diagnosis.
 XX Mus musculus.
 OS WO200047776-A2.
 PN 17-AUG-2000.
 PD 10-FEB-2000; 2000WO-US03515.
 PF 12-FEB-1999; 99US-0198248.
 PR 12-FEB-1999; 99US-0250125.
 XX (ZYMO) ZYMOGENETICS INC.

XX Jaspers SR, Whitmore TE, Conklin DC, Lofton-Day CE, Lok S;
 PI WPI; 2000-558220/51.
 XX N-PSDB; AAA50153.
 DR Identifying mutations in human chromosome 1p31, preferably a zins3 gene
 PT mutation, comprises using an insulin/relaxin family member (designated
 PT zins3), useful for diagnosing non-insulin dependent diabetes -
 XX Example 4; Page 46-47; 51pp; English.

XX The present sequence is that of a murine paralog (see AAY95771) of
 CC human zins3 (see AAY95770), a novel member of the insulin/relaxin
 CC family member that maps to a region of human chromosome 1 associated
 CC with non-insulin dependent diabetes mellitus (NIDDM). The sequence
 CC was deduced from an isolated cDNA clone (see AAA50153). Northern
 CC blots of embryo tissue indicated that mouse zins3 is expressed in
 CC a developmentally regulated fashion. zins3 polynucleotides and
 CC polypeptides can be used to diagnose disorders associated with
 CC abnormal expression of zins3, and to identify polymorphisms that
 CC result from mutations in the human zins3 gene. The invention
 CC provides methods for identifying abnormalities in expression that
 CC are a factor in causing, or predisposing, a person to some defect
 CC in glucose metabolism, such as NIDDM.

XX Sequence 135 AA;

Query Match 19.5%; Score 148; DB 21; Length 135;
 Best Local Similarity 29.9%; Pred. No. 2.8e-08;
 Matches 46; Conservative 21; Mismatches 51; Indels 36; Gaps 6;

QY 1 MARYMLLLAVVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGSRWRSDILAH 60

FT FT /note= "Given in SEQ ID NO 5"
 FT 53..54
 FT Region /label= C_peptide
 FT 55..118
 FT Region /note= "Claimed in claim 3"
 FT 55..114
 FT Cleavage-site 115..118
 FT /note= "Cleavage site at the junction of the C peptide
 FT and the A chain with a conserved RXRR motif"
 FT 119..142
 FT Region /label= A_chain
 FT 128..142
 FT Region /label= A_chain_consensus_sequence_region
 FT /note= "Given in SEQ ID NO 4"

WO200168862-A1.

XX 20-SEP-2001.
 XX 09-FEB-2001; 2001WO-US04199.
 XX 10-MAR-2000; 2000US-0523346.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Holloway JL, Lok S, Jaspers SR;
 PI WPI; 2001-582454/65.
 DR N-PSDB; AAH79088.

XX New insulin homologue polypeptide having homology to relaxin family,
 PT designated zins4 and zins4 polynucleotide, useful for diagnosing,
 PT preventing, treating reproductive, prostate, heart and kidney disorders
 PT -
 XX Claim 6; Page 72-73; 79pp; English.

XX The invention relates to an isolated insulin homologue zins4 having
 CC homology to the relaxin family. The zins4 gene, located on chromosome
 CC 1p31.1, encodes a 142 amino acid protein, where the zins4 polypeptide
 CC comprises a B chain and A chain comprising amino acid residues 26-52 and
 CC 119-142 respectively, joined by inter- and intra-chain disulfide bonds.
 CC zins4 has cytostatic, antifertility and vasotropic activity. zins4
 CC proteins are useful in applications for enhancing fertilisation during
 CC assisted reproduction in humans and animals and in therapies for treating
 CC reproductive disorders. zins4 protein is useful in treating reproductive,
 CC prostate, heart or kidney disorders and to identify cells, tissues or
 CC cell lines which respond to the zins4-stimulated pathway and to identify
 CC inhibitors of its activity. zins4 polypeptides and modulators of the
 CC polypeptide are useful in treating disorders associated with gonadal
 CC development, pregnancy, pubertal changes, menopause, ovarian cancer,
 CC polycystic ovarian syndrome and other reproductive functions including
 CC pathological conditions in ovary. Detection of zins4 polypeptides in the
 CC serum or tissue biopsy of a patient is useful for diagnosing ovarian
 CC cancer. The molecules are also useful for treating dysfunction associated
 CC with contractile tissues or to suppress or enhance contractility in vivo,
 CC treating cardiovascular disease, infertility, in vitro fertilization,
 CC birth control, treating impotence or other male reproductive dysfunction,
 CC inducing birth, for promoting growth, differentiation, development and/or
 CC maturation of ovarian cells, myocytes, endothelial cells, osteoblasts in
 CC culture and in the study of the ovarian cycle, reproductive function,
 CC ovarian cell-cell interactions and fertilisation. The polypeptide is also
 CC useful as a modulator of blood pressure, muscle tension and osmotic
 CC balance. The zins4 polynucleotide is useful in gene therapy.

XX Sequence 142 AA;

Query Match 100.0%; Score 760; DB 22; Length 142;
 Best Local Similarity 100.0%; Pred. No. 1e-74;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 lalflilvilav-----vevrsr-qtkkicgldyrtviycassrwrh----- 49
 QY 61 EAMGDTFFPDADADESLAGELDEAMGSSEWL-----ALTKSQAFYGRGPSWQ 108
 Db 50 --legfhfsqgaetrnylqlldrbepskktlehsplktdlsgqelvrdbqapkeg--lwe 105
 QY 109 GTPGVLRGSRDVLAGLSSSCCKWGCSSKSEISL 142
 Db 106 lkkhsvvrrd-----lqalcrcgcmkelstic 135

RESULT 3
 AAW37926
 ID AAW37926 standard; Protein; 135 AA.
 AC AAW37926;
 XX
 DT 01-SEP-1998 (first entry)
 DE Mouse Zins3 protein.
 XX
 KW Insulin homologue; identification; isolation; Zins3 receptor;
 KW treatment; disease; pre-elampsia; premature labour; Human.
 OS Mus sp.

Key Location/Qualifiers
 FT Peptide 23..48
 FT /note= "B chain"
 FT 49..115
 FT /note= "C-peptide"
 FT 116..135
 FT /note= "A chain"
 PN W09816635-A1.

XX 23-APR-1998.
 XX 15-OCT-1997; 97WO-US18593.
 XX 15-OCT-1996; 96US-0028177.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Conklin DC, Jaspers SR, Lofton-Day CE, Lok S;
 XX WPI; 1998-251285/22.
 XX N-PSDB; AAV29153.
 XX Insulin homologue polypeptide(s) and antagonists - used to, e.g.
 XX treat pre-elampsia, premature labour and Crohn's disease
 XX Claim 9; Page 67; 81pp; English.

CC The Zins3 protein is an insulin homologue protein. Polynucleotide
 CC molecules taken from its gene can be introduced into a cultured cell
 CC using an expression vector. The cell will express an insulin homologue
 CC polypeptide encoded by the polynucleotide. The polypeptides can also be
 CC expressed by introducing the polynucleotides into the germline of a
 CC nonhuman animal. The polypeptides can be used to identify and isolate
 CC receptors for zins3. Antibodies and antagonists of the polypeptides can
 CC be used for treating disease associated with extracellular matrix and
 CC vessels. The antibodies may also be used in the diagnosis of diseases
 CC associated with the polypeptide, such as reproductive disorders
 CC placental and colon pathology. Antagonists against the polypeptide may
 CC also be used to treat diseases such as preclampsia, premature labour, and
 CC Crohn's disease.

XX Sequence 135 AA;

Query Match 19.3%; Score 147; DB 19; Length 135;
 Best Local Similarity 29.9%; Pred. No. 3.6e-08;
 Matches 46; Conservative 21; Mismatches 51; Indels 36; Gaps 6;
 QY 1 MARYMLLLLVAVVLTGELWPCAEARAAPYGVRLCGREFIRAVITTCGSRWRSSDILAH 60
 Db 6 lalflilvilav-----vevrsr-qtkkicgldyrtviycassrwrh----- 49
 QY 61 EAMGDTFFPDADADESLAGELDEAMGSSEWL-----ALTKSQAFYGRGPSWQ 108
 Db 50 --legfhfsqgaetrnylqlldrbepskktlehsplktdlsgqelvrdbqapkeg--lwe 105
 QY 109 GTPGVLRGSRDVLAGLSSSCCKWGCSSKSEISL 142
 Db 106 lkkhsvvrrd-----lqalcrcgcmkelstic 135

RESULT 4
 AAW37925
 ID AAW37925 standard; Protein; 135 AA.
 AC AAW37925;
 XX
 DT 01-SEP-1998 (first entry)
 DE Human Zins3 protein.
 XX
 KW Insulin homologue; identification; isolation; Zins3 receptor;
 KW treatment; disease; pre-elampsia; premature labour; Human.
 OS Homo sapiens.

Key Location/Qualifiers
 FT Peptide 23..48
 FT /note= "B chain"
 FT 49..114
 FT /note= "C-peptide"
 FT 115..135
 FT /note= "A chain"
 PN W09816635-A1.

XX 23-APR-1998.
 XX 15-OCT-1997; 97WO-US18593.
 XX 15-OCT-1996; 96US-0028177.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Conklin DC, Jaspers SR, Lofton-Day CE, Lok S;
 XX WPI; 1998-251285/22.
 XX N-PSDB; AAV29150.
 XX Insulin homologue polypeptide(s) and antagonists - used to, e.g.
 XX treat pre-elampsia, premature labour and Crohn's disease
 XX Claim 2; Page 64-65; 81pp; English.

CC The Zins3 protein is an insulin homologue protein. Polynucleotide
 CC molecules taken from its gene can be introduced into a cultured cell
 CC using an expression vector. The cell will express an insulin homologue
 CC polypeptide encoded by the polynucleotide. The polypeptides can also be
 CC expressed by introducing the polynucleotides into the germline of a
 CC nonhuman animal. The polypeptides can be used to identify and isolate
 CC receptors for zins3. Antibodies and antagonists of the polypeptides can
 CC be used for treating disease associated with extracellular matrix and
 CC vessels. The antibodies may also be used in the diagnosis of diseases
 CC associated with the polypeptide, such as reproductive disorders
 CC placental and colon pathology. Antagonists against the polypeptide may
 CC also be used to treat diseases such as preclampsia, premature labour, and

PR	15-SEP-1999;	99WO-US21090.
PR	05-OCT-1999;	99WO-US23089.
XX	30-NOV-1999;	99WO-US28313.
PA	(GETH) GENENTECH INC.	
XX	Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, Wood WI;	
PI	Yuan J;	
XX		
DR	WPI; 2000-638201/61.	
DR	N-PSDB; AAA54109.	
XX		
PT	PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for	
PT	treating tumors including cancers of the breast and lung,	
PT	leukemia and for identifying compounds capable of inhibiting	
PT	growth of neoplastic cells	
XX		
PS	Claim 31; Fig 10; 133pp; English.	
XX		
CC	Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides	
CC	or their agonists (preferably anti-PRO agonist antibody or a small	
CC	molecule mimicking the biological activity of PRO polypeptide) are	
CC	useful in vitro or in vivo for inhibiting the growth of a tumour cell.	
CC	Compositions comprising the PRO polypeptides are useful for	
CC	inhibiting neoplastic cell growth and for treating cancer including	
CC	breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder,	
CC	central nervous system cancer, melanoma and leukaemia in a mammal.	
CC	The PRO polypeptides are also useful for treating other disorders	
CC	such as neuronal, glial, astrocytic, hypothalamic and other disorders	
CC	macrophagal, epithelial, stromal, blastocoelec disorders and	
CC	inflammatory, angiogenic and immunologic disorders and	
CC	useful for identifying agonists to PRO polypeptides as well as being	
CC	polypeptide with a candidate molecule and monitoring biological	
CC	activity mediated by the polypeptide.	
XX		
SQ	Sequence 135 AA;	
Query Match		
Best Local Similarity 16.6%; Score 126.5; DB 21; Length 135;		
Matches 41; Conservative 8; Mismatches 39; Indels 45; Gaps 5;		
QY	32 VRLCGREFIRAVITFCGSRWR-----SDILAH-----EAMGDTFPDA 70	
Db	: :	
QY	26 vrlcgleiyrtviycasswrhllegipqqaetgnsfqlphkrfseepaqnlpkv 85	
Db	: :	
QY	71 DAD-EDSLAGELDEAMGSSEWLALTKSPOAFYRGPRSMGTGPVLGRSDVLAGLSGCC 129	
Db	: :	
QY	86 dasgedrllwg-----gmpteeelwkskhsvmsrqd-----lqtllcc 122	
Db	: :	
QY	130 KWGCSSKSEISLCL 142	
Db	: :	
QY	123 tdgcsmtdlsalc 135	
Db	: :	
RESULT 7		
AAB24391		
ID	AAB24391 standard; Protein; 135 AA.	
AC	AAB24391;	
XX		
XX		
DT	07-NOV-2000 (first entry)	
XX		
DE	Human PRO182 protein sequence SEQ ID NO:16.	
XX		
KW	Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;	
KW	diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;	
KW	angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;	
KW	cystostatic; gene therapy; vaccine.	
OS	Homo sapiens.	
XX		
PN	WO200032221-A2.	

PT of ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228,
 PT PRO538, PRO172 or PRO182 polypeptide or their agonist
 XX
 PS Claim 14; Figure 10; 122pp; English.
 XX

CC Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182
 CC polypeptide or their agonists, mixed with a carrier is useful for
 CC inhibiting neoplastic growth and treating tumors such as cancers of
 CC breast, ovary, renal, colorectal, uterus, prostate, lung, bladder,
 CC central nervous system, melanoma and leukaemia.
 XX
 XQ Sequence 135 AA;

Query Match 16.6%; Score 126.5; DB 21; Length 135;
 Best Local Similarity 30.8%; Pred. No. 6.1e-06;
 Matches 41; Conservative 8; Mismatches 39; Indels 45; Gaps 5;
 QY 32 VRLCGREFIRAVITCGSRWRR-----SDILAH-----EAMGDTFPDA 70
 DB 26 VRLCGLEYIRTVIYICASSRWRRHLEGPQAQAGTNSFQLPHKREFSEENPAQNPVK 85
 QY 71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYGRPSWQTPGVLRGSRDVLAGLSSCC 129
 DB 86 dasgedrlwg-----gqmpeteelwskkshvmsrgd-----lqtlcc 122
 QY 130 KWGCSKSEISSLC 142
 DB 123 tdgcsmdtldsalc 135

RESULT 10
 AAM24033
 ID AAM24033 standard; Protein; 135 AA.
 XX
 AC AAM24033;
 XX

12-OCT-2001 (first entry)

Human EST encoded protein SEQ ID NO: 1558.

Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 diagnostics; forensic test; gene mapping; genetic disorder;
 biodiversity; gene therapy; nutrition.

Homo sapiens.

WO200154477-A2.

02-AUG-2001.

25-JAN-2001; 2001WO-US02687.

25-JAN-2000; 2000US-0491404.

17-JUL-2000; 2000US-0617746.

03-AUG-2000; 2000US-0631451.

15-SEP-2000; 2000US-0663870.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

Cao Y, Drmanac RA, Zhang J, Werhman T;

WPI; 2001-476164/51.

N-PSDB; AAH98692.

Isolated polypeptide for treatment of diseases, diagnostics, raising
 antibodies and research use

Claim 20; Page 1068-1069; 1275pp; English.

The present invention provides the protein and coding sequences of novel

CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a
 CC protein of the invention.
 XX
 XQ Sequence 135 AA;

Query Match 16.6%; Score 126.5; DB 22; Length 135;
 Best Local Similarity 30.8%; Pred. No. 6.1e-06;
 Matches 41; Conservative 8; Mismatches 39; Indels 45; Gaps 5;
 QY 32 VRLCGREFIRAVITCGSRWRR-----SDILAH-----EAMGDTFPDA 70
 DB 26 VRLCGLEYIRTVIYICASSRWRRHLEGPQAQAGTNSFQLPHKREFSEENPAQNPVK 85
 QY 71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYGRPSWQTPGVLRGSRDVLAGLSSCC 129
 DB 86 dasgedrlwg-----gqmpeteelwskkshvmsrgd-----lqtlcc 122
 QY 130 KWGCSKSEISSLC 142
 DB 123 tdgcsmdtldsalc 135

RESULT 11
 AAU12309
 ID AAU12309 standard; Protein; 135 AA.
 XX
 AC AAU12309;
 XX

24-OCT-2001 (first entry)

Human PRO182 polypeptide sequence.

Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 adipocyte; A-peptide; factor VIIA; gene therapy.

Homo sapiens.

WO200140466-A2.

07-JUN-2001.

01-DEC-2000; 2000WO-US32678.

01-DEC-1999; 99WO-US28301.

01-DEC-1999; 99WO-US28634.

02-DEC-1999; 99WO-US28551.

02-DEC-1999; 99WO-US28564.

02-DEC-1999; 99WO-US28565.

09-DEC-1999; 99US-0170262.

16-DEC-1999; 99WO-US30095.

20-DEC-1999; 99WO-US30911.

20-DEC-1999; 99WO-US30999.

30-DEC-1999; 99WO-US31243.

06-JAN-2000; 2000WO-US00277.

11-FEB-2000; 2000WO-US0376.

18-FEB-2000; 2000WO-US04341.

22-FEB-2000; 2000WO-US04342.

24-FEB-2000; 2000WO-US04414.

24-FEB-2000; 2000WO-US04914.

PR 01-MAR-2000; 2000WO-US05004.

PR 20-MAR-2000; 2000WO-US05601.

PR 21-MAR-2000; 2000WO-US07377.

PR 30-MAR-2000; 2000WO-US07532.

PR 30-MAR-2000; 2000WO-US08439.

XX 04-FEB-1992 (first entry)
 XX Sequence of human preprorelaxin H2.
 DE Relaxin; hormone; probe; uterine contraction.
 KW H2.
 XX
 OS

XX Key Location/Qualifiers
 FT Peptide 1..24
 FT Region /label= signal
 FT Region 25..57
 FT Region /label= B-chain
 FT Region 58..161
 FT Region /label= C-peptide
 FT Region 162..185
 FT Region /label= A-chain

XX EP112149-A.

XX 27-JUN-1984.

XX 12-DEC-1983; 83EP-0307553.

XX 13-DEC-1982; 82AU-0007247.

XX 09-DEC-1983; 83AU-0022283.

XX 01-JAN-1988; 88EP-0110103.

XX (FLOR-) FLOREY H INST EXPER.

XX (HOW-) HOWARD FLOREY INST.

XX Hudson PJ, Niall HD, Tregear GW;

XX WPI: 1984-160129/26.

XX N-PSDB; AAN40086.

XX Gene for expression of human H2-preprorelaxin - useful as vector

XX for prodn. of the peptide after expression etc.

XX Disclosure; Fig 2; 56pp; English.

XX The inventors claim a ds DNA SQ which comprises a coding strand and

XX a complementary strand corresp. to (AAN40086) and its subunits. Also

XX claimed are synthetic human H2-preprorelaxin, human H2-preprorelaxin

XX and human H2-relaxin together with their analogues having shortened A

XX or B chains, or modified to contain different AA residues.

XX Sequence 185 AA;

XX Query Match 14.7%; Score 111.5; DB 5; Length 185;

XX Best Local Similarity 22.7%; Pred. No. 0.00038;

XX Matches 42; Conservative 23; Mismatches 77; Indels 43; Gaps 4;

QY 1 MARYMLLLLLLAWVLTGELWPGCAARAAPYGVRLCGREFRAVIFTGSGSWRRSDILAH 60

DB 1 mprlffhllgvcllqngfsravadvmeevikicgrelvraqiaicgmstwsksrlsqe 60

QY 61 EAMGDTFPDADADESLAGELDEAMGSEWLA-----LTKS-----PQ----- 98

DB 61 dapqprpvaievpvsnfinkdtetinnmefvanlpqelkltlsemqpalpqlqhvvpvlk 120

QY 99 -----AFYGRPS-----WOGTPGVLRGSRDVLAGLSSSCCKWGCKSKSE 137

DB 121 dsallfeefkllnrqseadspsskylgldthsrkrqlysalankcchvgctkrs 180

QY 138 ISSLC 142

DB 181 larfc 185

RESULT 15
 AAP94621
 ID AAP94621 standard; protein; 185 AA.
 XX
 AC AAP94621;
 XX
 DT 21-JUN-1990 (first entry)
 XX
 DE Amino acid sequence of human preprorelaxin H2.

XX Relaxin; H2-relaxin; pubic symphysis.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..25
 FT Peptide /label=Signal peptide
 FT Peptide 26..57
 FT Peptide /label=B-chain
 FT Peptide 58..161
 FT Peptide /label=C-peptide
 FT Peptide 162..159
 FT Peptide /label=A-chain

XX EP303033-A.

XX 15-FEB-1989.

XX 12-DEC-1983; 83EP-0110103.

XX 13-DEC-1982; 82AU-0007247.

XX (FLOR-) FLOREY H INST EXPER.

XX Hudson PJ, Tregear GW, Niall HD;

XX WPI: 1989-047874/07.

XX N-PSDB; AAN92483.

XX New human H2-relaxin analogues -

XX with shortened and/or modified A and/or B chains.

XX Disclosure; ; 25pp; English.

XX "H2" relaxin is deduced from a cDNA clone, has the general properties of

XX a growth factor and is capable of altering nature of connective tissue

XX and inducing smooth muscle contraction, specifically during labour.

XX Sequence 185 AA;

XX Query Match 14.4%; Score 109.5; DB 10; Length 185;

XX Best Local Similarity 22.7%; Pred. No. 0.00062;

XX Matches 42; Conservative 22; Mismatches 78; Indels 43; Gaps 4;

QY 1 MARYMLLLLLLAWVLTGELWPGCAARAAPYGVRLCGREFRAVIFTGSGSWRRSDILAH 60

DB 1 mprlffhllgvcllqngfsravadvmeevikicgrelvraqiaicgmstwsksrlsqe 60

QY 61 EAMGDTFPDADADESLAGELDEAMGSEWLA-----LTKS-----PQ----- 98

DB 61 dapqprpvaievpvsnfinkdtetinnmefvanlpqelkltlsemqpalpqlqhvvpvlk 120

QY 99 -----AFYGRPS-----WOGTPGVLRGSRDVLAGLSSSCCKWGCKSKSE 137

DB 121 dsallfeefkllnrqseadspsskylgldthsrkrqlysalankcchvgctkrs 180

QY 138 ISSLC 142

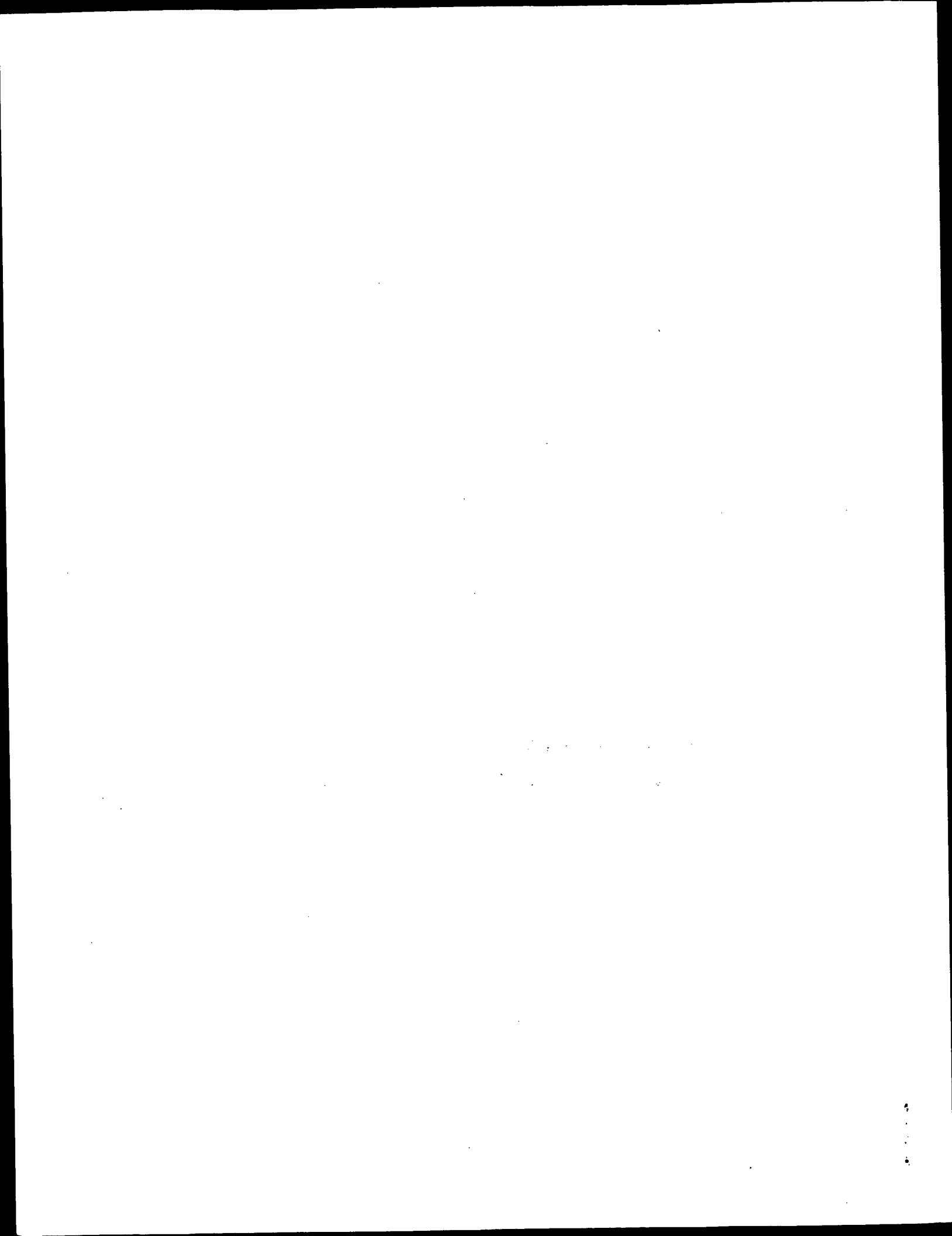
DB 181 larfc 185

• Fri Jun 28 11:32:00 2002

Search completed: June 27, 2002, 16:08:08
Job time: 277 sec

us-09-781-077-2.rag

Page 11



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2002, 16:05:31 ; Search time 28.78 seconds
(without alignments)
120.515 Million cell updates/sec

Title: US-09-781-077-2
Perfect score: 760
Sequence: 1 MARYMLLLVAVLTGELW.....GLSSCKKWCCKSEITSLC 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6ptodata/2/1aa/PTUS_COMB.pep.*
6: /cgn2_6ptodata/2/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	148	19.5	135	3	US-08-950-720A-6
2	126.5	16.6	135	3	US-08-950-720A-2
3	116	15.3	130	6	5464756-16
4	109.5	14.4	185	3	US-08-950-720A-12
5	107.5	14.1	162	6	5464756-18
6	102.5	13.5	164	6	5464756-20
7	102	13.4	29	6	5464756-15
8	98.5	13.0	185	3	US-08-950-720A-13
9	98	12.9	77	1	US-08-443-568B-10
10	98	12.9	77	5	PCT-US94-06997-10
11	95	12.5	101	3	US-08-950-720A-14
12	92.5	12.2	40	2	US-08-353-476-92
13	89.5	11.8	150	5	US-08-443-568B-12
14	89.5	11.8	150	5	PCT-US94-06997-12
15	88.5	11.6	134	4	US-09-201-226-2
16	88.5	11.6	188	4	US-08-905-267-2
17	88.5	11.6	188	4	US-09-314-051-2
18	84.5	11.1	110	3	US-08-950-720A-11
19	84.5	11.1	110	3	US-08-589-028-2
20	84.5	11.1	110	3	US-08-784-582-2
21	84.5	11.1	110	4	US-08-785-271-2
22	84.5	11.1	110	5	PCT-US95-08596-2
23	79.5	10.5	1070	4	US-08-697-954-2
24	76	10.0	31	2	US-08-484-219-4
25	76	10.0	213	2	US-08-905-267-13
26	76	10.0	213	4	US-09-314-051-13
27	74.5	9.8	24	6	5464756-8

28	73	9.6	32	6	5464756-11
29	72	9.6	33	6	5464756-10
30	72	9.5	174	3	US-08-911-853-19
31	72	9.5	174	4	US-09-479-409-19
32	72	9.5	174	4	US-09-479-453-19
33	71.5	9.4	110	3	US-08-589-028-4
34	71.5	9.4	110	3	US-08-784-582-4
35	71.5	9.4	110	4	US-08-785-271-4
36	71	9.3	29	1	US-08-443-568B-2
37	71	9.3	29	2	US-08-484-219-5
38	71	9.3	29	5	PCT-US94-06997-2
39	71	9.3	33	2	US-08-353-476-90
40	71	9.3	52	1	US-08-443-568B-14
41	71	9.3	52	5	PCT-US94-06997-14
42	69	9.1	94	1	US-07-989-845-28
43	69	9.1	94	1	US-07-989-844-12
44	69	9.1	94	1	US-08-161-044-12
45	69	9.1	94	1	US-08-240-121-12

ALIGNMENTS

RESULT 1
US-08-950-720A-6
; Sequence 6, Application US/08950720A
; Patent No. 6046028
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Lok, Si
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: INSULIN HOMOLOG
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,720A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-950-720A-6

Query Match 19.5% Score 148; DB 3; Length 135;

Best Local Similarity 29.9%; Pred. No. 1.3e-09;
Matches 46; Conservative 21; Mismatches 51; Indels 36; Gaps 6;

QY 1 MARYMLLLAVVWLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
Db 6 LALFLLVLLAV-----VEVRSR-QTVKLCGLDYVRTVIYICASSRWRH-----49

QY 61 EAMGDTFPDADDSLAGELDEAMGSSEWL-----ALTKSPQAFYRGRPSWQ 108
Db 50 --LEGHFSQQAETRNVLQLDRHPSKKTLEHSLPKTDLGQGLVDRDQAPKEG--LWE 105

QY 109 GTPGVLRGSRDVLGLSSCKKWCCKSEISSLC 142
Db 106 LKHVVSVRRD----LQALCCGCGCKMKELSTLC 135

RESULT 2
US-08-950-720A-2
; Sequence 2, Application US/08950720A
; Patent No. 6046028
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Lok, Si
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: INSULIN HOMOLOG
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,720A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-950-720A-2

Query Match 16.6%; Score 126.5; DB 3; Length 135;
Best Local Similarity 30.8%; Pred. No. 3.9e-07;
Matches 41; Conservative 8; Mismatches 39; Indels 45; Gaps 5;

QY 32 VRLCGREFIRAVIFTCGGSRWRR-----SDILAH-----EAMGDTFPDA 70
Db 26 VRLCGLEVIRTVIVICASSRWRHLEGIPOAQQAETGNSQLPKHREFSEENPAQLPKV 85

QY 71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQTPGVLRGSRDVLGLSSCC 129
Db 86 DASGEDRLWG-----GQMPTEELWKKSHSVMSRQD-----LQTLCC 122

QY 130 KWGCKSEISSIC 142
Db 123 TDGCSMTDLSALC 135

RESULT 3
5464756-16
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:16:
; LENGTH: 30
5464756-16

Query Match 15.3%; Score 116; DB 6; Length 30;
Best Local Similarity 86.4%; Pred. No. 8.8e-07;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 31 GVRLCGREFIRAVIFTCGGSRW 52
Db 9 GIKLCGREFIRAVIYTCGGSRW 30

RESULT 4
US-08-950-720A-12
; Sequence 12, Application US/08950720A
; Patent No. 6046028
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Lok, Si
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: INSULIN HOMOLOG
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,720A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672

; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046028e
; US-08-950-720A-12

Query Match 14.4%; Score 109.5; DB 3; Length 185;
Best Local Similarity 22.7%; Pred. No. 5.3e-05;
Matches 42; Conservative 22; Mismatches 78; Indels 43; Gaps 4;
QY 1 MARYMLLLAVVLTGELWPGAEARAPYVGLCGREFIRAVFTCGGSRWRSDILAH 60
Db 1 MPRLLFFHLLGVCLLLNQFRAVADSMVEEVIKLGRRLVRAQIAICGMSTWKSRLSQE 60
QY 61 EAMGDTTPDADADESLAGELDEAMGSSEWLA-----LTKS-----PQ----- 98
Db 61 DAPOTPRVAEIVPSFINKDTETINMMSEFVANLPQELKLTLSMQPALPOLQOHVPVVK 120
QY 99 -----AFYGRPS-----WQGTGVLGRSDVLAGLSSCKCKWGCKSE 137
Db 121 DSSLFEEFKKLIRNQSEADSSPSLKYLGLDTHSRKKRLQYALANKCCHVGCTKRS 180
QY 138 ISSIC 142
Db 181 LARFC 185

RESULT 5
5464756-18
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:18:
; LENGTH: 162
5464756-18

Query Match 14.1%; Score 107.5; DB 6; Length 162;
Best Local Similarity 23.4%; Pred. No. 7.6e-05;
Matches 36; Conservative 20; Mismatches 55; Indels 43; Gaps 4;
QY 32 VRLCGREFIRAVFTCGGSRWRSDILAHAMGDTFPDADADESLAGELDEAMGSSEWL 91
Db 9 IKLCGRELVRQAIAICGMSTWKSRLSQEDAPQTPRPVAEIVPSFINKDTETINMMSEFV 68
QY 92 A-----LTKS-----PQ-----AFYGRPS-----WQ 108
Db 69 ANLPQELKLTLSMQPALPOLQOHVPVLDSSLLFEEFKKLIRNQSEADSSPSLKYL 128
QY 109 GTPGVLRGRSDVLAGLSSCKCKWGCKSEISLCL 142
Db 129 GLDTHSRKKRLQYALANKCCHVGCTKRLARFC 162

RESULT 6
5464756-20
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,

; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:20:
; LENGTH: 164
5464756-20

Query Match 13.5%; Score 102.5; DB 6; Length 164;
Best Local Similarity 22.4%; Pred. No. 0.00029;
Matches 35; Conservative 20; Mismatches 56; Indels 45; Gaps 4;
QY 32 VRLCGREFIRAVFTCGGSRWRSDILAHAMGDT-----FPDADADESLAGEL 81
Db 9 IKLCGRELVRQAIAICGMSTWKSRLSQEDAPQTPRPVAEIVPSFINKDTETINMMSEF 68
QY 82 DEAMGSSEWLA LTKSPOA-----FYGRPS-----W 107
Db 69 VANLPQELKLTLSMQPALPOLQOHVPVLDSSLLFEEFKKLIRNQSEADSSPSLKY 128
QY 108 GTPGVLRGRSDVLAGLSSCKCKWGCKSEISLCL 142
Db 129 GLDTHSRKKRLQYALANKCCHVGCTKRLARFC 164

RESULT 7
5464756-15
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:15:
; LENGTH: 29
5464756-15

Query Match 13.4%; Score 102; DB 6; Length 29;
Best Local Similarity 81.0%; Pred. No. 3.4e-05;
Matches 17; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 31 GVRLCGREFIRAVFTCGGSR 51
Db 9 GIKLCGREFIRAVFTCGGSR 29

RESULT 8
US-08-950-720A-13
; Sequence 13, Application US/08950720A
; Patent No. 6046028
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Lok, Si
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: INSULIN HOMOLOG
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.

COUNTRY: U. S. A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,568B
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/080,354
FILING DATE: 21-JUNE-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B.
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 7842-037
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ID: 08-08-443-568B-10

[illegible]

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10
RESULT
PCT-US94-06997-10
; Sequence 10, Application PC/TUS9406997
;
; GENERAL INFORMATION:
;
; APPLICANT: Genentech, Inc.
; APPLICANT: 460 Point San Bruno Boulevard
; APPLICANT: South San Francisco, California
; APPLICANT: United States of America
;
; TITLE OF INVENTION: Process for Producing Relaxin
;
; NUMBER OF SEQUENCES: 37
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: pennie & Edmonds
;
; STREET: 1155 Avenue of the Americas
;
; CITY: New York
;
; STATE: New York
;
; COUNTRY: U.S.A.
;
; ZIP: 10036
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: PCT/US94/06997
;
; FILING DATE: 20-JUN-1994
;
; CLASSIFICATION:
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Halluin, Albert P.

```

STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq for Windows Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6046028e
SS-08-950-720A-13

Query Match	13.0%;	Score 98.5;	DB 3;	Length 185;	
Best Local Similarity	23.8%;	Pred. NO. 0.00098;			
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	1 :	:	:	:	:
1 MPRLFLHLLFCLLNQFSAVAAKWDVKLCGRFLVRAQIATCGMSTWSKRSQEQ 60					
	1 :	:	:	:	:
	1 :	:	:	:	:
61 EAMGDTFPDAD-----ADEDS-----LACELDEAMGSEMI-----ALT 94					
	1 :	:	:	:	:
	1 :	:	:	:	:
61 DAQPTPRVAEIVPSFNKDTETIIIMLEFIANLPPELKAALSERQPSLPELQQIVPAIK 120					
	1 :	:	:	:	:
	1 :	:	:	:	:
95 KSPQAF-----YGRGSP-----WQGTGPGVLGRSDRVLAGLSSCKCKWGCKSE 137					
	1 :	:	:	:	:
	1 :	:	:	:	:
121 DSNLSFEFFKKLIIRNQSEAADNPSELKYLGLDTHSQKKRRPYVALFEKCLIGCTKRS 180					
	1 :	:	:	:	:
	1 :	:	:	:	:
138 ISSLC 142					
	1 :	:	:	:	:
	1 :	:	:	:	:
181 LAKYC 185					
	1 :	:	:	:	:
	1 :	:	:	:	:

```

RESULT          9
US-08-443-568B-10
; Sequence 10, Application US/08443568B
; Patent No. 5759807
; GENERAL INFORMATION:
; APPLICANT: Breece, Tim
; APPLICANT: Haysenga, Kirk
; APPLICANT: Rindersknecht, Ernst
; APPLICANT: Vandien, Richard
; APPLICANT: Daniel, Yansura
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York

```


us-09-781-077-2.rai

Page 7

QY	6	LLLLLAVVLITGELWPGAEARAAPYGVRLCGREFIRAVITFCGS	---RRRRSDILAHEA	62
Db	10	LLLLLLAT---ASQLQPVQGR	---KMGCEALLQALDVICVNGFTTRVRRVRSASKDAR	61
QY	63	MGDTF-----PDADADSDLSLAGEAMGSSSEWIALTKSPQAFYGRPQWGTGVLGRS	117	
Db	62	VNDLIRKLQOPDEIEQETETGLKQKHTDAD-----TEKGVPPAVGSGRKLRRH	111	
QY	118	RDVLAGLSSSCCKWGCCKSEISLC	142	
Db	112	RRRIA---HECCKEGCTDIDLVC	133	

Search completed: June 27, 2002, 16:08:44
Job time: 193 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2002, 16:05:56 ; Search time 36.01 Seconds
(without alignments)
378.914 Million cell updates/sec

Title: US-09-781-077-2

Perfect score: 760

Sequence: 1 MARYMLLLAVVLTGELW.....GLSSCCCKWGCSEISL 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	153	20.1	54	2	A26463	relaxin - spiny dogfish
2	117	15.4	44	1	RXRKOT	relaxin - sand tig
3	109.5	14.4	185	1	A60982	relaxin 2 precursor
4	108.5	14.3	166	2	S42786	relaxin 2 precursor
5	106.5	14.0	182	1	RXPQ	relaxin precursor
6	102	13.4	131	2	A53024	Leydig insulin-like
7	101.5	13.4	185	2	A34936	relaxin precursor
8	100.5	13.2	64	2	A29543	relaxin - little s
9	99	13.0	131	2	B53024	Leydig insulin-like
10	99	13.0	185	2	S48082	relaxin precursor
11	98.5	13.0	185	1	A44559	relaxin 1 precursor
12	98	12.9	186	1	RXRT	relaxin precursor
13	95.5	12.6	166	2	S42783	relaxin 1 precursor
14	89.5	11.8	59	2	A53879	relaxin - dog (fra
15	88	11.6	145	2	S43224	insulin-related pr
16	86.5	11.4	57	2	S42784	relaxin - gorilla
17	86.5	11.4	178	2	A49014	20K protein - rabb
18	84.5	11.1	110	1	IPHU	insulin precursor
19	83.5	11.0	110	2	A42179	insulin precursor
20	82.5	10.9	139	2	A83140	hypothetical prote
21	80.5	10.6	110	2	JO0178	insulin precursor
22	80	10.5	106	2	AD0408	conserved hypothet
23	80	10.5	187	2	T10897	insulin-like growt
24	78.5	10.3	54	2	B32201	relaxin - minke wh
25	78.5	10.3	110	2	B42179	insulin precursor
26	78	10.3	116	1	IPAF	insulin precursor
27	78	10.3	2591	2	T30288	pristinamycin I sy
28	77	10.1	143	2	I47053	relaxin B,C and A
29	77	10.1	2129	2	T14182	fbx protein - Myc

30 77 10.1 2569 2 T14164 peptide synthetase
31 76.5 10.1 48 2 A49739 relaxin - horse (f
32 76.5 10.1 108 2 A39883 insulin precursor
33 76.5 10.1 115 1 IPHF insulin precursor
34 76.5 10.1 380 2 C83171 conserved hypothet
35 76 10.0 513 1 RGECAV transcription regu
36 76 10.0 513 2 F90866 hypothetical prote
37 76 10.0 513 2 C85752 conserved hypothet
38 75.5 9.9 319 2 D75349 insulin-like growt
39 75 9.9 663 2 C70838 probable zinc meta
40 75 9.9 667 2 C87236 probable zinc meta
41 75 9.8 576 2 S33327 catalase (EC 1.11.
42 74.5 9.7 54 2 A32201 relaxin - Bryde's
43 73.5 9.7 107 1 IPCH insulin precursor
44 73.5 9.7 109 1 IPRTDU insulin precursor
45 73 9.6

ALIGNMENTS

RESULT 1
A26463
relaxin - spiny dogfish (fragments)
C:Species: Squalus acanthias (spiny dogfish)
C:Date: 19-Nov-1988 #sequence_revision 26-May-1995 #text_change 26-May-1995
C:Accession: B26463; A26463
R:Bullesbach, E.E.; Gowan, L.K.; Schwabe, C.; Steinetz, B.G.; O'Byrne, E.; Callard, Eur. J. Biochem. 161, 335-341, 1986
A:Title: Isolation, purification, and the sequence of relaxin from spiny dogfish (Sq
A:Reference number: A91179; MUID:87054035
A:Accession: B26463
A:Molecule type: protein
A:Residues: 'E', 2-30 <BUIL>
A:Experimental source: ovary
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we
A:Accession: A26463
A:Molecule type: protein
A:Residues: 31-54 <B02>
A:Experimental source: ovary
C:Superfamily: insulin
C:Keywords: hormone; pyroglutamic acid
F:1-30/31-54/Product: relaxin #status experimental <MAT>
F:1-30/Domain: chain B #status experimental <CHB>
F:31-54/Domain: chain A #status experimental <CHA>
F:1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental
F:13-41,25-54,40-45/Disulfide bonds: #status predicted

Query Match 20.1%; Score 153; DB 2; Length 54;
Best Local Similarity 28.6%; Pred. No. 5.2e-08;
Matches 32; Conservative 10; Mismatches 4; Indels 66; Gaps 2;

QY 31 GVRLCGRFTRAVFTCGSRWRSDILAHEAMGTFPDADADESLAGELDEAMGSEW 90
Db :|||||:|||||:|||||
9 GIKLCGRFTRAVFTCGSR-----

QY 91 LALTKSPQAFYGRGRSGWGTGVLGRSDVLGLSSCCCKWGCSEISL 142
Db :|||:|||||:|||||
30 -----WEGSP-----GMSRCKCTGYCTRKDISILC 54

RESULT 2

RXRKOT

relaxin - sand tiger (tentative sequence) (fragments)

C:Species: Odontaspis taurus (sand tiger)

C:Date: 01-Sep-1981 #sequence_revision 26-May-1995 #text_change 31-Mar-2000

C:Accession: A01616

R.Gowan, L.K.; Reinig, J.W.; Schwabe, C.; Bedarkar, S.; Blundell, T.L.

FEBS Lett. 129, 80-82, 1981

A:Title: On the primary and tertiary structure of relaxin from the sand tiger shark

A:Reference number: A01616; MUID:82004703

A:Accession: A01616

A: Molecule type: protein
A: Residues: 1;2-19;21-44 <GOW>
R: Bullesbach, E.E.; Gowan, L.K.; Schwabe, C.; Steinetz, B.G.; O'Byrne, E.; Callard, I.P.
Eur. J. Biochem. 161, 335-341, 1986
A: Title: Isolation, purification, and the sequence of relaxin from spiny dogfish (Squalus
A: Reference number: A91179; MUID: 87054035
A: Contents: annotation; sequence revision
A: Note: the carboxyl-terminal sequence of chain B was determined to be Arg-Trp
C: Superfamily: insulin
C: Keywords: pyroglutamic acid
F: 1-19/Domain: chain B (#status experimental <CHB>
F: 21-44/Domain: chain A (#status experimental <CHA>
F: /Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F: /Disulfide bonds: 20-35/Disulfide bonds: #status predicted

```

Query Match      15.4%; Score 117; DB 1; Length 44;
Best Local Similarity 24.5%; Pred. No. 0.00013;
Matches 27; Conservative 6; Mismatches 11; Indels 66; Gaps 1;

y 33 RLCGRFTRVIFTCGSRWRRSDILAHEAMGDTFFDADADESLAGELDEAMGSEWLA 92
      ||||| ||||| || ||||| |
b 1 QLCGRGFTRAFIFACGGSRWATS-----23
      ||||| ||||| || ||||| |

y 93 LTKSPQAFYRGRPSWQGTGGVLRSDRVLAGLSGCCCKWCCSKSEJSLC 142
      : || ||||| : |||||
24 -----PAMSTKCYIGCTRKDISVLC 44

```

RESULT 3.
60982 elaxin 2 precursor [validated] - human
elaxin 2 precursor [validated] - human
;Alternate names: preprorelaxin 2
;Species: Homo sapiens (man)
;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 08-Dec-2000
;Accession: A05092; A60982
;Author: Hudson, P.; John, M.; Crawford, R.; Haralambidis, J.; Gorman, J.; Tregear,
J.M.D. J. 3, 2333-2339, 1984
;Title: Relaxin gene expression in human ovaries and the predicted structure of a human
relaxin precursor. PMID:85051298
;Reference number: A05092; MUID:85051298
A;Accession: A05092
Molecule type: mRNA
Residues: 1-185 <HMD>
Cross-references: GB:X00948; NID:g35926; PIDN:CAA25460.1; PID:g35927
Stults, J.T.; Bourell, J.H.; Canova-Davis, E.; Ling, V.T.; Laramsee, G.R.; Winslow, J.W
Environ. Mass Spectrom. 19, 655-664, 1990
;Title: Structural characterization by mass spectrometry of native and recombinant huma
relaxin. Reference number: A60982; MUID:91167739
A;Accession: A60982
Molecule type: protein
Residues: 25-53;162-185 <STU>

C:Genetics:
A:Gene: GDB:RLN2
A:Cross-references: GDB:119553; OMIM:179740
A:Map position: 9pter-9q12
C:Superfamily: insulin
C:Keywords: ovary; pyroglutamic acid
F:1-34/Domain: signal sequence #status predicted <SIG>
F:25-53/Domain: relxin 2 chain B #status experimental <BCH>
F:25-53,162-185/Product: relxin 2 #status experimental <MAT>
F:58-157/Domain: relxin 2 connecting C peptide #status predicted <CPEP>
F:162-185/Domain: relxin 2 chain A #status experimental <ACH>
F:35-172,47-185,171-176/Dissulfide bonds: #status experimental
F:162/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experimental

Query Match	14.4%	Score 109.5;	DB 1;	Length 185;
Best Local Similarity	22.7%	pred. No. 0.0028		
		22. Mismatches	78:	
			Indels	43: Gaps
				4:

Qy 1 MARYMLLLLVVWVLTGELWPCAERAAPYGVRLCGRFIRAVIFTCGSRWRRSDILAH 60

```

-98 -----PQ-----LTKS-----
61 EMAGDTFFDADADEDSLACELDEAMGSSEWLA:::| | | | |
Db : | | | | | | | | | | |
61 DAPOTPRVAEIVPSFINKDTETINNSEFVANLPQBELKLTISEMOPALPOLQORHPVLK 120
      : | | | | | | | | | | |
Qy 99 -----AFYGRGPS-----WGTFGVLRGSRDVLACLSSCCCKGCSCSKSE 137
      : | | | | | | | | | | |
Db 121 DSLLFEFKKLIRNQSEAADSPELSKLYGLDTHSRKKRQLYSALANKCCHVCTKRS 180
      : | | | | | | | | | | |
Qy 138 ISSLC 142
      :: |
Db 181 LARFC 185

RESULT 4
relaxin 2 precursor - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1995
A:Accession: S42786
R:Evans, B.B.
submitted to the EMBL Data Library, November 1993
A:Reference number: S42776
A:Accession: S42786
A:Molecule type: mRNA
A:Residues: 1-166 <EVA>
A:Cross-references: EMBL:Z27245; NID:g416109; PIDN:CAA81758.1; PID:g416110
C:Genetics:
A:Gene: rlx2
A:Superfamily: insulin
F:1-5/Domain: signal sequence (fragment) #status predicted <SIG>
F:1-5/Domain: signal sequence (fragment) #status predicted <MAT>
```

[illegible]

RESULT 5
RXPG
relaxin precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 18-Jun-1999
C:Accession: A09034; A931187; A90205; A90196; S32312; A29796; A01615
R:Haley, J.; Hudson, P.; Scanlon, D.; John, M.; Shine, J.; Tregear, G.; Ni
DNA 1, 155-162, 1982
A:Title: Porcine relaxin: molecular cloning and cDNA structure.
A:Reference number: A90934; MUID:83157118
A:Accession: A90934
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-182 <HAL>
A:Cross-references: GB>K01088; NID:g164634; PIDN:AAA31114.1; PID:g164635
R:James, R.; Niall, H.; Kwok, S.; Bryant-Greenwood, G.
Nature 267, 544-546, 1977
A:Title: Primary structure of porcine relaxin: homology with insulin and related growth
A03187. MUID:77213057

A; Accession: A93187
A; Molecule type: protein
A; Residues: 25-50, 'TWGR'; 161-182 <JAM>
A; Residues: J.K.: Steinetz, B.G.
Gibson C.: McDonald.

10

QY 93 -----LTKSPQAFYR-----GRPSWQCTPGV-----LRGSRDVLGLSSCCCKW 131
 Db 114 HAPVLSDSVVSLGFKTLHLRDLGEADGSPGLKYLQSDTHSRKKRSGGLMSQCCCHV 173
 QY 132 GCKSKSETSSL 141
 Db 174 GCSRRSTAKL 183

RESULT 11

A44559
 relaxin 1 precursor - human
 N:Alternate names: preprorelaxin 1
 C:Species: Homo sapiens (man)
 C:Date: 03-Feb-1994 #sequence_revision 07-Oct-1994 #text_change 18-Jun-1999
 R:Accession: B05092; A44559
 R:Hudson, P.; John, M.; Crawford, R.; Haralambidis, J.; Gorman, J.; Tregear, EMO J. 3, 2333-2339, 1984
 A:Title: Relaxin gene expression in human ovaries and the predicted structure of a human
 A:Reference number: A05092; MUID:85051298
 A:Accession: B05092
 A:Molecule type: DNA
 A:Residues: 1-185 <HU1>
 A:Cross-references: GB:X00949; NID:g35932; PIDN:CAA25461.1; PID:g35933
 R:Hudson, P.; Haley, J.; John, M.; Cronk, M.; Crawford, R.; Haralambidis, J.; Tregear, EMO J. 3, 628-631, 1983
 A:Title: Structure of a genomic clone encoding biologically active human relaxin.
 A:Reference number: A44559; MUID:83141755
 A:Accession: A44559
 A:Molecule type: DNA
 A:Residues: 1-185 <HU2>
 A:Cross-references: GB:X00949; NID:g35932; PIDN:CAA25461.1; PID:g35933
 C:Comment: Relaxin is an ovarian hormone that acts with estrogen to produce dilation of
 disulfide bonds.
 C:Genetics:
 A:Gene: GDB:RLM1
 A:Cross-references: GDB:119552; OMIM:179730
 A:Map position: 9pter-9q12
 C:Superfamily: insulin
 C:Keywords: hormone; ovary
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-57/Domain: relaxin 1 chain B #status predicted <BCH>
 F:58-162/Domain: relaxin 1 #status predicted <MAT>
 F:163-185/Domain: relaxin 1 connecting C peptide #status predicted <CPEP>
 F:35-172,47-185,171-176/Disulfide bonds: #status predicted <ACH>

Query Match 13.0%; Score 98.5; DB 1; Length 185;
 Best Local Similarity 23.8%; Pred. No. 0.032; Mismatches 19; Indels 43; Gaps 5;
 Matches 44; Conservative 19;

QY 1 MARYMLLLLVVLTGELWPGAEARAPYGVRLCGREFIRAVFTCGSRWRSDILAH 60
 Db 1 MPRFLFHLLEFCLLNQFSRAVAARKDDVIKLCGRVLRQAICGMSWTSKRSLSQE 60
 QY 61 EAMGDTFPDAD-----ADEDS-----LAGELDEAMGSEWL-----ALT 94
 Db 61 DAPQTPRPVAEIVPSPINKDTETIIMLEFANLPPELKAALSERQPSLPELQOYVPALK 120
 QY 95 KSPQAF-----YRGRPS-----WQGTGVLGRSDVLGLSSCCCKWCKSKSE 137
 Db 121 DSNLSEEPFKLIRNRQSEADSNPSELKYLGLDTHSQKKRRPYVALFEKCLIGCTKRS 180
 QY 138 ISSLC 142
 Db 181 LAKYC 185

RESULT 12

RAT
 relaxin precursor - rat
 C:Species: Rattus norvegicus (Norway rat)

C:Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 24-Sep-1999
 C:Accession: A01614
 R:Hudson, P.; Haley, J.; Cronk, M.; Shine, J.; Niall, H.
 Nature 291, 127-131, 1981
 A:Title: Molecular cloning and characterization of cDNA sequences coding for rat relaxin
 A:Reference number: A01614; MUID:81197624
 A:Accession: A01614
 A:Molecule type: mRNA
 A:Residues: 1-186 <HUD>
 A:Cross-references: GB:J00780; GB:M25468; NID:g206606; PIDN:AAA42029.1; PID:g206607
 C:Superfamily: insulin
 C:Keywords: hormone; ovary; pyroglutamic acid
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-57/Domain: relaxin chain B #status predicted <RXB>
 F:58-162/Domain: relaxin #status predicted <MAT>
 F:163-186/Domain: relaxin connecting C peptide #status predicted <RXC>
 F:36-173,48-186,172-177/Disulfide bonds: #status predicted <RXA>
 F:163/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted

Query Match 12.9%; Score 98; DB 1; Length 186;
 Best Local Similarity 23.8%; Pred. No. 0.036;
 Matches 45; Conservative 25; Mismatches 69; Indels 50; Gaps 8;

QY 1 MARYMLLLLVVLTGELWPGAEARAA----PYGVRLCGREFIRAVFTCGSRWR---53
 Db 1 MSSRLLLQLLGFWFLFSQ---PCARVSEWMDQVITQVCGRYARAVIEVCGASVGRALAL 57
 QY 54 ---RSDIILAHAMGDTFP---DADADE-----PSLAGELDEAMG-----86
 Db 58 SQEPAPLARQATAEVVPSPINKDAEPDFTLCLPNLSEERKAALSEGRRAPPELQOHA 117
 QY 87 ---SSEWLALTKSPQAFYR-----GRP--SWQGTGVLGRSDVLGLSSCCCKWGC 133
 Db 118 PALSDSVVSLGEGPKTFHNLGEADGPGPELKYLGSDAQSRKKRQSGALLSEQCCHIGC 177
 QY 134 SKSEISSLC 142
 Db 178 TRRSIAKLC 186

RESULT 13

S42783
 relaxin 1 precursor - chimpanzee (fragment)
 C:Species: Pan troglodytes (chimpanzee)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
 C:Accession: S42783
 R:Evans, B.B.
 submitted to the EMBL Data Library, November 1993

A:Reference number: S42776
 A:Accession: S42783
 A:Molecule type: mRNA

A:Residues: 1-166 <EVA>
 A:Cross-references: EMBL:Z27225; NID:g415996; PIDN:CAA81739.1; PID:g415997
 C:Genetics:
 A:Gene: r1x1
 A:Superfamily: insulin
 C:Keywords: disulfide bond; hormone
 F:1-5/Domain: signal sequence (fragment) #status predicted <SIG>
 F:16-166/Product: relaxin 1 #status predicted <MAT>

Query Match

Best Local Similarity 12.6%; Score 95.5; DB 2; Length 166;
 Matches 36; Conservative 18; Mismatches 55; Indels 47; Gaps 5;

QY 32 VRLCGREFIRAVFTCGSRWRSDIILAHAMGDTFPDAD-----ADED-----75
 Db 13 IKLCGRVLRQAICGMSWTSKRSLSQEDAPQTPRPVAEIVPSPINKDTETIIMLEPT 72
 QY 76 -SLAGELDEAMGSEWLALTKSPQAF-----YRGRPS-----106

Db 73 ANLPPELKAAL--SERQPSLPEQQYVPALKDNLNLSFEFPFKLIIRNQSEADSNPSELK 130

QY 107 WQGTGVLGRSDVLGLAGLSSCKKWCSEISLCL 142

Db 131 YLGLDTHSQKRRQPYVALFEKCCLLIGCTKRLANVC 166

RESULT 14

A53879
relaxin - dog (fragments)
C:Species: Canis lupus familiaris (dog)
C:Date: 27-Sep-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C:Accession: B53879; A53879
R:Stewart, D.R.; Henzel, W.J.; Vandlen, R.
J. Protein Chem. 11, 247-253, 1992
A:Title: Purification and sequence determination of canine relaxin.
A:Reference number: A53879; MUID:93000391
A:Accession: B53879

A:Molecule type: protein
A:Residues: 1-35 <STE>
A:Experimental source: placenta
A:Note: sequence extracted from NCBI backbone (NCBIP:115401)
A:Accession: A53879
A:Molecule type: protein
A:Residues: 36-59 <ST2>
A:Experimental source: placenta
A:Note: sequence extracted from NCBI backbone (NCBIP:115399)
C:Superfamily: insulin
C:Keywords: hormone
F:1-35,36-59/Product: relaxin #status experimental <MAT>
F:1-35/Domain: chain B #status experimental <CHB>
F:36-59/Domain: chain A #status experimental <CHA>
F:9-46,21-59,45-50/Disulfide bonds: #status predicted

Query Match 11.8%; Score 89.5; DB 2; Length 59;
Best Local Similarity 20.7%; Pred. NO. 0.075;
Matches 23; Conservative 11; Mismatches 20; Indels 57; Gaps 2;

QY 32 VRLCGREFIRAVFTCGGSEWRSDILAEHMGDTFPDADADEDSLAGEDEAMGSSEWL 91

Db 6 LKAGRDYVRLQIEVCGSSWNGRK-----AQQLRE----- 35

QY 92 ALTKSPQAFYGRPSWQGTGVLGRSDVLGLAGLSSCKKWCSEISLCL 142

Db 36 -----DNVIMSKDCCNVGCTRRRELASRC 59

RESULT 15

S43224
insulin-related protein precursor - migratory locust
C:Species: Locusta migratoria (migratory locust)
C:Date: 28-Sep-1994 #sequence_revision 12-Apr-1996 #text_change 12-Jun-1998
C:Accession: S43224; S07774; S07773; S17851; S42153
R:Kromer-Metzger, E.; Lagueux, M.
Eur. J. Biochem. 221, 427-434, 1994
A:Title: Expression of the gene encoding an insulin-related peptide in Locusta (Insecta).
A:Reference number: S43224; MUID:94222089
A:Accession: S43224
A:Molecule type: DNA
A:Residues: 1-145 <KRO>
A:Cross-references: EMBL:229963
R:Lagueux, M.; Lwoff, L.; Meister, M.; Goltzene, F.; Hoffmann, J.A.
Eur. J. Biochem. 187, 249-254, 1990
A:Title: cDNAs from neurosecretory cells of brains of Locusta migratoria (Insecta, Orthoptera).
A:Reference number: S07774; MUID:90126827
A:Accession: S07774
A:Molecule type: mRNA
A:Residues: 1-131,133-145 <LAG>
A:Cross-references: EMBL:X17024; NID:99529; PID:g9530
R:Hieter, H.; van Dorsselaer, A.; Green, B.; Denoroy, L.; Hoffmann, J.; Luu, B.
Eur. J. Biochem. 187, 241-247, 1990
A:Title: Isolation and structure elucidation of a novel 5-kDa peptide from neurohaemal

A:Reference number: S07773; MUID:90126826

A:Accession: S07773
A:Molecule type: protein
A:Residues: 67-116 <HIE>
R:Heru, C.; Li, K.W.; Bulet, P.; Lagueux, M.; Hoffmann, J.A.
Eur. J. Biochem. 201, 495-499, 1991
A:Title: Isolation and structural characterization of an insulin-related molecule, a
A:Reference number: S17851; MUID:92037603
A:Accession: S17851
A:Molecule type: protein
A:Residues: 34-64;123-143 <HET>
C:Genetics:
A:Introns: 70/1
F:1-22/Domain: signal sequence #status predicted <SIC>
F:34-64/Product: insulin-related protein chain B #status experimental <BCH>
F:67-116/Product: connecting peptide #status experimental <PEP>
F:123-143/Product: insulin-related protein chain A #status experimental <ACH>

Query Match 11.6%; Score 88; DB 2; Length 145;
Best Local Similarity 26.7%; Pred. No. 0.26;
Matches 39; Conservative 28; Mismatches 59; Indels 20; Gaps 8;

QY 6 LLLLLLVWVLT-----GELWPGAEARA-APYGV-RLCGREFIRAVFTCGGSRMRSDIL 58

Db 8 LLAVLAVCLSTATQOSDLFLLSPKRSQAPQVARYCGEKLNALKLVCRGN----YNTM 63

QY 59 AHEAMGDTFPDADADEDSLAGEDEAMGSSEWLALTKSPQAFYGRPSWQGTGVLGRS- 117

Db 64 FKKASQDV-SDSESDNYWGSQSADEAAEAALPPYP-----ILARPS---AGLLTGAV 116

QY 118 -RDVLAGLSSCKKWCSEISLCL 142

Db 117 FRRRTGTVFDECCRKSCSISELQTYC 142

Search completed: June 27, 2002, 16:09:27
Job time: 211 sec

1. The first part of the document is a list of the names of the persons who were present at the meeting. The names are listed in alphabetical order.

Fri Jun 28 11:32:02 2002

OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20191540; PubMed=10727251;
 RA Hombach-Klonisch S., Abd-Elnaem M., Skidmore J.A., Leiser R.,
 RA Fischer B., Klonisch T.; pregnant one-humped camel.;
 RT "Ruminant relaxin in the pregnant one-humped camel."
 RL Biol. Reprod. 62:839-846 (2000).
 CC -1- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 DR EMBL: AF254739; AAF67741.1; -;
 DR HSP; P01348; IRLX.
 DR InterPro: IPR000739; Insulin_IGF_relaxin.
 DR SMART: SM00078; IIGF; 1.
 DR PROSITE: PS00262; INSULIN; 1. F69BBD7E4FA8089 CRC64;
 SQ SEQUENCE 199 AA; 22386 MW; 22386 MW;

Query Match 13.6%; Score 103.5; DB 6; Length 199;
 Best Local Similarity 18.1%; Pred. No. 0.0096;
 Matches 39; Conservative 24; Mismatches 62; Indels 91; Gaps 4;

QY 1 MARYMLLLAVVWLTGELWPGAEARAAPYVRLCGREFTRAVFTCGGSRWRR-----54
 Db 1 MPRLLSHLLGVWLLLSQLPKTSERSNDFVKACGRVRLWIEICGSYSWGPRPRA 60
 QY 55 -----SDLAHE-----AMG 64
 Db 61 PRAPKALPALPALSODKKPRLRSPPAIEIMPSSITTKDAETLTMTLETPNLQELTATLS 120
 QY 65 DTFPPDADDEDLAG-----ELDEAMSGSEWALTCKSPQAFYGRPS 106
 Db 121 ERQPSAEQPPAKDNLNFEFFKFIIDRQNEEDSELKLNGLDKHSEK-----173
 QY 107 WQGTGVLGRSDVLGAGLSSCKCKGWSKSEISSLC 142
 Db 174 -----KRLQWTLGERCCQKGSRKEMATAC 199

RESULT 4
 Q9GK47 PRELIMINARY; PRT; 131 AA.
 ID Q9GK47
 AC Q9GK47
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RELAXIN-LIKE PROTEIN.
 OS Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.
 OX NCBI_TaxID=9463;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RA Klonisch T., Froehlich C., Tetens F., Fischer B., Hombach-Klonisch S.;
 RA "Molecular remodeling of members of the relaxin family during primate
 evolution."
 RT Mol. Biol. Evol. 0:0-0(2001).
 RL -1- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 DR EMBL: AF317624; AAG42317.1; -;
 DR InterPro: IPR000739; Insulin_IGF_relaxin.
 DR SMART: SM00078; IIGF; 1.
 DR PROSITE: PS00262; INSULIN; 1.
 SQ SEQUENCE 131 AA; 14414 MW; F18AFA9ACFC85943 CRC64;

Query Match 13.3%; Score 101; DB 6; Length 131;
 Best Local Similarity 24.5%; Pred. No. 0.01; Indels 60; Gaps 8;
 Matches 39; Conservative 15; Mismatches 45;

QY 1 MARYMLLLAVVWLTGELWPGAEARAAPYVRLCGREFTRAVFTCGGSRWRRSDI 57
 Db 1 MRLFLSHLLGVWLL-----SLRARKIPAEVLRKACGRVRLQIRICGSLSGWKSQ 55
 QY 58 LAHEAMGDTFFDADDEDLAGELDEAMSGSEWL-----ALTKSPQAFYGRPSWQ 108
 Db 56 QHREPRQAPALPEIVSSITSGAELNGMLEYIPDLQELKATLSEREPFRELQPSLK 115
 QY 109 GP-----PGVL-----RGRDVLGAGLSSCKCKGWSKSE 137
 Db 116 DSNLNEVEKSIILGRQNEAEDQSLGRLSRDLAHSRIKRSYIRYSDRCNVGTRKE 175
 QY 138 ISSLC 142
 Db 176 LADLC 180

RESULT 3
 Q9N0T9 PRELIMINARY; PRT; 199 AA.
 ID Q9N0T9
 AC Q9N0T9
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PREPRORELAXIN.

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QY 10 LAVW--VLTC-----ELWPCAARAAPYGVRLCGREFIRAVITFCGSRWRSDILAHEA 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5 LSWALVLGLPALVFAHPSLSLETR-----KLCGHFHFVRLVRLCGPRWS----- 52
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 63 MGDTPDADADESLAGELDEAMGSSEW-----ALTKSPQAPYRG 103
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 53 -----PEAGT-----SSAGGDELL-----QWLERPHILHGLVAHDPALVGLQPLPOASHH 101
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 104 RPSWQGTGVLGRSDVLAGLSSCKKWKSCSEISSLC 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 102 -----RHRAAATNPAAHRCCLSGCTRODLLTLC 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
Q9N0T8 ID Q9N0T8 PRELIMINARY; PRT; 131 AA.
AC Q9N0T8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RELAXIN-LIKE PROTEIN.
OS Dama dama (Fallow deer) (Cervus dama).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=30532;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20150568; PubMed=10687860;
RA Hombach-Klonisch S., Kauffold J., Rautenberg T., Steger K., Tetens F.,
RA Fischer B., Klonisch T.;
RT "Relaxin-like factor (RLF) mRNA expression in the fallow deer.";
RL Mol. Cell. Endocrinol. 159:147-158(2000).
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR EMBL; AF254740; AAF67742.1;
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR SMART; SM00078; IIGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
SQ SEQUENCE 131 AA; 14406 MW; EC7731679E60B0C7 CRC64;

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Query Match 12.9%; Score 98; DB 6; Length 131;
Best Local Similarity 27.7%; Pred. No. 0.021;
Matches 36; Conservative 17; Mismatches 43; Indels 34; Gaps 7;

QY 23 AEARAPYGVRLCGREFIRAVITFCGSRWRSDILAHEAMGDTFPDADADES---LAG 79
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 24 AAQEVF--EKLCGHFHFVRLVRLCGPRW-----SSDRPVAGGDELLRWLEG 72
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 80 E--LDEAMGSSE--WALTKSPQA--FYGRPSWQGTGVLGRSDVLAGLSSCKKWK 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 73 QHLLHGLMASGDPVLVLAPOPLFQASRRHHRRATAINP-----ARHCCLSG 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 133 CSKSEISSLC 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 120 CTRODLLTLC 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
Q9N0Z8 ID Q9N0Z8 PRELIMINARY; PRT; 131 AA.
AC Q9N0Z8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RLF.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=99260294; PubMed=10331451;
RA Hombach-Klonisch S., Tetens F., Kauffold J., Steger K., Fischer B.,
RA Klonisch T.;
RT "Molecular cloning and localization of caprine relaxin-like factor
RT (RLF) mRNA within the goat testis.";
RL Mol. Reprod. Dev. 53:135-141(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Hombach-Klonisch S., Klonisch T.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR EMBL; AF233686; AAF60301.1;
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR Pfam; PF00049; Insulin; 1.
DR SMART; SM00078; IIGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
SQ SEQUENCE 131 AA; 14160 MW; 2A82EB59EA07313A CRC64;

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Query Match 11.6%; Score 88; DB 6; Length 131;
Best Local Similarity 21.4%; Pred. No. 0.22;
Matches 33; Conservative 14; Mismatches 25; Indels 82; Gaps 5;

QY 23 AEARAPYGVRLCGREFIRAVITFCGSRWRSDILAHEAMGDTFPDADADESLAGELD 82
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 24 AAQEVF--EKLCGHFHFVRLVRLCGPRW-----SSDRPVAGGDELLRWLEG 51
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 83 EAMGSSEWALTKSPQAFYGRPSWQGTGVLGR--GSRDVLGLSSS----- 127
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 52 -----SSE-----SGRPVAGGDELLRWLEGQHLHGLMASGDPVLVLAPOPLP 95
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 128 -----CCKWGCSEISSLC 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 96 QASRRHHRRATAINPARHCCCLSGCTRODLLTLC 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 7
Q9GK46 ID Q9GK46 PRELIMINARY; PRT; 188 AA.
AC Q9GK46;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PRORELAXIN.
OS Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.
OX NCBI_TaxID=9463;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYONIC TROPHOBLAST, PLACENTA;
RA Klonisch T., Froehlich C., Tetens F., Fischer B., Hombach-Klonisch S.;
RT "Molecular remodeling of members of the relaxin family during primate
RT evolution.";
RL Mol. Biol. Evol. 0:0-0(2001).
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR EMBL; AF317625; AAG42318.1;
DR HSP; P04090; 6RLX.
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR SMART; SM00078; IIGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
SQ SEQUENCE 188 AA; 21573 MW; 77551629B82B9A66 CRC64;

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Query Match 11.3%; Score 86; DB 6; Length 188;
Best Local Similarity 21.3%; Pred. No. 0.52;
Matches 43; Conservative 21; Mismatches 64; Indels 74; Gaps 8;

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QY 1 MARYMLLLLVVLTGELWPAEARA-APYGVRL-----CGREFIRAVIFTCG--GSR 51
DB 1 MPRLLFFHLLGVWLLLLQI-----SRAMDKNGENLQIIPACGRRLIRLWVEVCGSTGFR 55
QY 52 WRRSDILAH-----EAMGDTFFPDADADESLAGELDEAMGSSWALTKSPQAFYRG 103
DB 56 GRANKOTEHQPGSEFPSEIIPSPFINKDAETINN-----MSEFIANLPQKQKTTQS 106
QY 104 R-----PSWQOTPGVLRS-----RDV 120
DB 107 EMNLPSPLOQYPTPLKSGDISFEEYKNNIHNEQGEADNSHSELQNLGLDTHSRKKRER 166
QY 121 LAGLSSSCCKWGCKSKSEISSIC 142
DB 167 YMSPLQKCCRIGCTYKRSIARFC 188
RESULT 8
Q9HWY2 PRELIMINARY; PRT; 139 AA.
AC Q9HWY2
DT 01-MAR-2001 (TRENBLrel. 15, Created)
DT 01-MAR-2001 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2001 (TRENBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN PA4046.
GN PA4046.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
Hickey M.J., Brinkman F.S.D., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltz L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen";
RL Nature 406:959-964(2000).
DR EMBL; AF004821; AAG07433.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 139 AA; 15161 MW; 9F5D69D2981A389A CRC64;
Query Match 10.9%; Score 82.5; DB 16; Length 139;
Best Local Similarity 26.0%; Pred. No. 0.83; Indels 27; Gaps 4;
Matches 34; Conservative 14; Mismatches 56;
QY 6 LLLLLLVVLTGELWPAEARAAPYGVRLCGREFIRAVIFTCGSRWRRSDILAHEAMGD 65
DB 22 LPLLIIVFEFLEQLPLHGLAMPFIALLSMFVNPLF---GAYKRLIATQKA--- 74
QY 66 TFPDADADESLAGELDEAMGSEW--LALTKSPQAFYRGPSWQGPV---LRGSRDV 120
DB 75 -----LDTAEAAWTRLAQVRRKRALFGSLPAWIGVPGFAGLNGVALI 119
QY 121 LAGLSSSCCKW 131
DB 120 LIGVLSLVFW 130
RESULT 9
Q9ND22 PRELIMINARY; PRT; 1722 AA.
AC Q9ND22
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

POSSIBLE SERINE PROTEASE.
DE L4325.06.
GN Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FRIEDLIN;
RA Oliver K., Harris D., Ivens A.C., Quail M., Rajandream M.A.,
Barrell B.G.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=FRIEDLIN;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AL356713; CAB92392.1; -.
DR MEROPS; S08.UPW; -.
DR InterPro; IPR000209; Peptidase_S8.
DR Pfam; PF00082; Peptidase_S8; 2.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Protease.
SQ SEQUENCE 1722 AA; 182741 MW; 8148DD78AC52DDIF CRC64;
Query Match 10.7%; Score 81; DB 5; Length 1722;
Best Local Similarity 24.4%; Pred. No. 23;
Matches 32; Conservative 15; Mismatches 40; Indels 44; Gaps 7;
QY 10 LAVVVLVGTGEL---WPGAERAAAPYGVRLCGREFIRAVIFTCGSRWRRSDILAHEAMGD 66
DB 1507 LLLMLHTNLNHRWDSALQ-----CEARRWARA---RHRSTADT 1543
QY 67 FPDADA-DEDSLAGEAMGSSS-----WLALTKSPQAFYRGPSW--QGTP 111
DB 1544 TFGDSVGVDRKAANFDEVLGTAFRAHVGVVGRWLWASLVESTE---RDAASFVEGPE 1600
QY 112 GVLGRGSRDLA 122
DB 1601 DETRFQDYAA 1611
RESULT 10
O57687 PRELIMINARY; PRT; 187 AA.
AC O57687;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE IGF-II PRECURSOR.
GN IGF-2.
OS Taenopygia guttata.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea; Passeridae;
OC Taenopygia.
OX NCBI_TaxID=72052;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=EMBRYO;
RA Holzenberger M.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=EMBRYO;
RX MEDLINE=97426547; PubMed=9278533;
RA Holzenberger M., Jarvis E.D., Chang C., Grossman M., Nottebohm F.,
Scharff C.;
RT "Selective expression of insulin-like growth factor II in the song
bird brain.";


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RL J. Neurosci. 17:6974-6987(1997).
CC -|- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
DR EMBL; AJ223165; CAA11145.1; -.
DR HSSP; P01344; IGF2.
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR Pfam; PF00049; Insulin; 1.
DR PRINTS; PR00276; INSULIN.
DR PRINTS; PR00277; INSULINB.
DR ProDom; PD001048; Insulin_IGF_relaxin; 1.
DR SMART; SM00078; IIGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW SIGNAL.
FT CHAIN.
FT CHAIN.
SQ SEQUENCE 187 AA; 20908 MW; 3C7EAD8F7D2CE8F CRC64;

Query Match
Best Local Similarity 23.1%; Score 80; DB 13; Length 187;
Matches 33; Conservative 8; Mismatches 38; Indels 64; Gaps 4;

QY 2 ARYMILLLLAVVLTGELWPGAEARAAPYGV--RLCGREFIRAVITCGGSRWRSDILA 59
Db 11:||||| 11:|||||
4 ARRMILLLLAFAY-----AMDSAAAYGTAETLCGGELVDTLQFVCG----- 45
QY 60 HEAMGDTFPDADADESLAGELDEAMGSSEWALTGPSQAFYGRPSWQGTGVLGRSD 119
Db 46 -----DRGFYFSRP-----VGRNRR 61

QY 120 VLAGLSSCCCKGCKSKSEISLC 142
Db 62 FNRGIVECCFRSCDLALLETC 84

RESULT 11
ID P79890 PRELIMINARY; PRT; 187 AA.
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE PREPRO-INSULIN-LIKE GROWTH FACTOR-II.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96397665; PubMed=8804558;
RA Darling D.C., Brickell P.M.;
RT "Nucleotide sequence and genomic structure of the chicken insulin-like
growth factor-II (IGF-II) coding region.";
CC Gen. Comp. Endocrinol. 102:283-287(1996).
CC -|- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR EMBL; S82962; BAB46818.1; -.
DR EMBL; S82960; BAB46818.1; JOINED.
DR HSSP; P01344; IGF2.
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR Pfam; PF00049; Insulin; 1.
DR PRINTS; PR00276; INSULIN.
DR PRINTS; PR00277; INSULINB.
DR ProDom; PD001048; Insulin_IGF_relaxin; 1.
DR SMART; SM00078; IIGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
SQ SEQUENCE 187 AA; 20837 MW; B301581CD4878EEC CRC64;

Query Match
Best Local Similarity 10.5%; Score 80; DB 13; Length 187;
Matches 32; Conservative 10; Mismatches 37; Indels 64; Gaps 4;

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QY 2 ARYMILLLLAVVLTGELWPGAEARAAPYGV--RLCGREFIRAVITCGGSRWRSDILA 59
Db 11:||||| 11:|||||
4 ARQIILLLLAFAY-----ALDSAAAYGTAETLCGGELVDTLQFVCG----- 45
QY 60 HEAMGDTFPDADADESLAGELDEAMGSSEWALTGPSQAFYGRPSWQGTGVLGRSD 119
Db 46 -----DRGFYFSRP-----VGRNRR 61

QY 120 VLAGLSSCCCKGCKSKSEISLC 142
Db 62 INRGIVECCFRSCDLALLETC 84

RESULT 12
ID Q9FLA4 PRELIMINARY; PRT; 1429 AA.
AC Q9FLA4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE POLYPROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98344145; PubMed=9679202;
RA Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
features of the regions of 1,381,565 bp covered by twenty one
RL DNA Res. 5:131-145(1998).";
DR EMBL; AB010693; BAB10876.1; -.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00098; zf-CCHC; 1.
DR SMART; SM00343; Znf_C2HC; 1.
DR zinc-finger.
SQ SEQUENCE 1429 AA; 159492 MW; 7B20CCFB1A9BC263 CRC64;

Query Match
Best Local Similarity 10.5%; Score 80; DB 10; Length 1429;
Matches 39; Conservative 16; Mismatches 39; Indels 56; Gaps 8;

QY 22 GAERAAAPYGVRLCGREFIRAVITCGGSRWRSDILAHEAMGDTFPDADADES----- 76
Db 1151 GIEATRTSRGLHLMQRIY-----TDLKKHNMMLDTPVSTPSPPTKLSL 1196
QY 77 LAG-ELDEA-----MGSEWALTGPSQAF-----YGRPS-----WQGTGVLGRSD 119
Db 1197 LSGTALDDATEYRTVLGSLQYLAFTPDIAFANRLSQFMRHPTNEHWOAKRIILR----- 1252
QY 120 VLAGLSS-----SCCKWGC 133
Db 1253 YLAGTSHGIFLRSDFLTTHAFSDADWGC 1282

RESULT 13
ID Q9FF95 PRELIMINARY; PRT; 542 AA.
AC Q9FF95;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE SIMILARITY TO UNKNOWN PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).

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us-09-781-077-2.rspt

Page 7

Search completed: June 27, 2002, 16:16:28
Job time: 497 sec

1. The first part of the document is a list of the names of the persons who were present at the meeting. The names are listed in alphabetical order.

Fri Jun 28 11:32:02 2002

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Query Match      19.5%; Score 148; DB 1; Length 135;
Best Local Similarity 29.9%; Pred. No. 1,le-07;
Matches 46; Conservative 21; Mismatches 51; Indels 36; Gaps 6;

ID INL5_MOUSE STANDARD; PRT; 135 AA.
AC Q9W0G6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Insulin-like peptide INSUL5 precursor (Insulin-like peptide 5).
DE (Relaxin/insulin-like protein) (Relaxin/insulin-like factor 2).
DE INSL5 OR ZINS3 OR RIF2 OR RIF.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Colon;
RX MEDLINE=99389725; PubMed=10458910;
RA Conklin D., Lofton-Day C.E., Haldeman B.A., Ching A., Whitmore T.E.,
RA Lok S., Jaspers S.;
RT "Identification of INSUL5, a new member of the insulin superfamily.";
RL Genomics 60:50-56(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB; TISSUE=Ovary;
RX MEDLINE=20065648; PubMed=10598589;
RA Hsu S.Y.;
RT "Cloning of two novel mammalian paralogs of relaxin/insulin family
RT proteins and their expression in testis and kidney.";
RL Mol. Endocrinol. 13:2163-2174(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX Strausberg R.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAY HAVE A ROLE IN GUT CONTRACTILITY OR IN THYMIC
CC DEVELOPMENT AND REGULATION.
CC -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN COLON WITH LOWER LEVELS
CC IN THYMUS. MINIMAL LEVELS IN TESTIS.
CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC
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CC
CC EMBL; AF133817; AAD29687.1;
CC DR EMBL; AF076971; AAD48089.1;
CC DR EMBL; AF054842; AAF09093.1; ALT_INIT.
CC DR EMBL; AF054843; AAF09094.1;
CC DR EMBL; BC010968; AAH10968.1;
CC DR MGD; MGI:1346085; Insl5.
CC DR InterPro; IPR000739; Insulin_IGF_relaxin.
CC DR SMART; SM00262; ILGF; 1.
CC DR PROSITE; PS00262; Hormone; Signal.
CC KW Insulin family; Hormone; Signal.
CC FT SIGNAL 1 22
CC FT CHAIN 23 135
CC FT INSULIN-LIKE PEPTIDE INSUL5 B CHAIN
CC FT CONNECTING PEPTIDE (POTENTIAL).
CC FT (POTENTIAL).
CC FT INSULIN-LIKE PEPTIDE INSUL5 A CHAIN
CC FT (POTENTIAL).
CC FT INSULIN-LIKE PEPTIDE INSUL5 B CHAIN
CC FT (POTENTIAL).
CC FT PROPEP 49 114
CC FT CHAIN 115 135
CC FT DISULFID 29 122
CC FT DISULFID 41 135
CC FT DISULFID 121 126
CC FT BY SIMILARITY.
CC FT SEQUENCE 135 AA; 15524 MW; 05FF9A0F613DBF92 CRC64;

RESULT 3
INL5_HUMAN STANDARD; PRT; 135 AA.
ID INL5_HUMAN
AC Q9Y5Q6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Insulin-like peptide INSUL5 precursor (Insulin-like peptide 5).
DE INSL5.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Colon;
RX MEDLINE=99389725; PubMed=10458910;
RA Conklin D., Lofton-Day C.E., Haldeman B.A., Ching A., Whitmore T.E.,
RA Lok S., Jaspers S.;
RT "Identification of INSUL5, a new member of the insulin superfamily.";
RL Genomics 60:50-56(1999).
CC -1- FUNCTION: MAY HAVE A ROLE IN GUT CONTRACTILITY OR IN THYMIC
CC DEVELOPMENT AND REGULATION.
CC -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGLY EXPRESSED IN RECTUM WITH LOWER LEVELS
CC IN UTERUS AND ASCENDING AND DESCENDING COLON.
CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC
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CC
CC EMBL; AF133816; AAD29686.1;
CC DR MIN; 606413;
CC DR InterPro; IPR000739; Insulin_IGF_relaxin.
CC DR SMART; SM00078; ILGF; 1.
CC DR PROSITE; PS00262; INSULIN; 1.
CC KW Insulin family; Hormone; Signal.
CC FT SIGNAL 1 18
CC FT CHAIN 19 48
CC FT INSULIN-LIKE PEPTIDE INSUL5 B CHAIN
CC FT (POTENTIAL).
CC FT INSULIN-LIKE PEPTIDE INSUL5 A CHAIN
CC FT (POTENTIAL).
CC FT PROPEP 49 114
CC FT CHAIN 115 135
CC FT DISULFID 29 122
CC FT DISULFID 41 135
CC FT DISULFID 121 126
CC FT BY SIMILARITY.
CC FT SEQUENCE 135 AA; 15318 MW; 98FFCB20E9C4BC1F CRC64;

```

[illegible]

Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
[1]
SEQUENCE FROM N.A.
TISSUE=Placenta;
MEDLINE=99150177; PubMed=10026098;
Klonisch T., Hombach-Klonisch S., Froehlich C., Kauffold J.,
Steger K., Steinetz B.G., Fischer B.;
"canine preprorelaxin: nucleic acid sequence and localization within
the canine placenta.";
Biol. Reprod. 60:551-557(1999).
[2]
SEQUENCE OF 26-60 AND 154-177.
TISSUE=Placenta;
MEDLINE=93000391; PubMed=1388669;
Stewart D.R., Henzel W.J., Vandlen R.;
"Purification and sequence determination of canine relaxin.";
J. Protein Chem. 11:247-253(1992).
!- FUNCTION: Relaxin-

relaxin is an ovarian hormone that acts with estrogen to produce dilation of the birth canal in many mammals.

- !- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.
- !- SUBCELLULAR LOCATION: Secreted.
- !- TISSUE SPECIFICITY: Placenta; syncytiotrophoblast.
- !- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

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EMBL; AF233687; AAF63032.1; -
HSPSP; P01348; 4RLX.
InterPro: IPR000739; Insulin_IGF_relaxin.
Pfam; PF000449; Insulin; 1.
SMART; SM00078; ILGF; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Signal.
SIGNAL 1 25
CHAIN 26 60
PROPEP 63 149
CHAIN 154 177
DISULFID 34 164
RELAXIN B CHAIN.
CONNECTING PEPTIDE (BY SIMILARITY).
RELAXIN A CHAIN.
INTERCHAIN

DISULFID	163	168	
CONFLICT	49	49	
SEQUENCE	177 AA;	20563 MW;	220BB0EC99DD302A CRC64;
Query Match		14.8%	Score 112.5; DB 1; Length 177;
Best Local Similarity			

Query Match 14.88; Score 112.5; DB 1; Length 177;
Best Local Similarity 21.5%; Pred. No. 0.00041;
Matches 43; Conservative 16; Mismatches 60; Indels 81; Gaps 4;

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DR InterPro: IPR000739; Insulin_IGF_relxin.
 DR Pfam: PF00049; Insulin; 1.
 DR SMART: SM00078; IIGF; 1.
 DR PROSITE: PS00262; INSULIN; 1.
 KW Insulin family; Hormone; Signal.
 FT SIGNAL 1 25
 FT CHAIN 26 53 RELAXIN B CHAIN.
 FT PROPEP 54 156 CONNECTING PEPTIDE.
 FT CHAIN 161 182 RELAXIN A CHAIN.
 FT DISULFID 35 169 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 47 182 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 168 173 BY SIMILARITY.
 FT CONFLICT 66 66 A -> V (IN REF. 2).
 FT CONFLICT 133 133 L -> Q (IN REF. 2).
 SQ SEQUENCE 182 AA; 20721 MW; E5C941430A838B8 CRC64;

Query Match 14.5%; Score 110; DB 1; Length 182;

Best Local Similarity 21.8%; Pred. No. 0.00074;
Matches 41; Conservative 25; Mismatches 70; Indels 52; Gaps 6;

QY 1 MARYMLLLAVVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGSRWRSIDILAH 60
 DB 1 MRRFLSHVGLNWLSSQLPRELSQKPDVVKACGRELARLRIEIGCSLSWKTVLRLE 60
 QY 61 EAMGDTFPDADADE-----DSLAGEIDAMGSSEWL--ALTKSPQAFYRGR-PSW----- 107
 DB 61 E-----PGLEAGQPVEIVSSISKDAEALNKLGLNSLNFKEQKATLSERQPSWRELLQ 114
 QY 108 -----QGTPGVLRGRSDV-----LAGLSSSCCKWGCS 134
 DB 115 QPALKDSNLEEFEEETILKTQSEVEDDLSLKNLGLDKHRSRKRMTQLSHKCCYWGCT 174
 QY 135 KSEISLCL 142
 DB 175 RKELARQC 182

RESULT 7

REL2_HUMAN STANDARD; PRT; 185 AA.
 ID REL2_HUMAN
 AC P04090; Q9UCX3; Q99936;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Prolaxin H2 precursor.
 GN RN2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
 RX MEDLINE=85051298; PubMed=6548702;
 RA Hudson P., John M., Crawford R., Haralambidis J., Scanlon D.,
 RA Gorman J., Tregear G., Shine J., Niall H.;
 RT "Relaxin gene expression in human ovaries and the predicted structure
 of a human preprorelaxin by analysis of cDNA clones.";
 RL EMBO J. 3:2333-2339(1984).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RA Sehra H.;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 RP PARTIAL SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
 RP SPECIFICITY.
 RC TISSUE=Prostate;
 RX MEDLINE=96328899; PubMed=8735594;
 RA Gunnarsen J.M., Fu P., Roche P.J., Tregear G.W.;
 RT "Expression of human relaxin genes: characterization of a novel
 alternatively-spliced human relaxin mRNA species.";
 RL Mol. Cell. Endocrinol. 118:85-94(1996).
 [4]

RESULT 6

RELX_HORSE STANDARD; PRT; 182 AA.
 AC P22969; Q28907;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Prolaxin precursor (RXN).
 GN RN.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=HOKAIDO; TISSUE=Placenta;
 RA Min K., Shiota K., Ogawa T.;
 RT "Molecular cloning of equine preprorelaxin cDNA.";
 RL J. Reprod. Dev. 42:171-178(1996).
 [2]
 RP SEQUENCE OF 32-174 FROM N.A.
 RX TISSUE=Placenta;
 RA MEDLINE=95359320; PubMed=7543295;
 RA Klonsch T., Ryan P.L., Yamashiro S., Porter D.G.;
 RT "Partial complementary deoxyribonucleic acid cloning of equine relaxin
 messenger ribonucleic acid, and its localization within the equine
 placenta.";
 RL Biol. Reprod. 52:1307-1315(1995).
 [3]
 RP SEQUENCE OF 26-53 AND 163-182.
 RX TISSUE=Placenta;
 RA MEDLINE=91275796; PubMed=2055195;
 RA Stewart D.R., Nevins B., Hadas E., Vandlen R.;
 RT "Affinity purification and sequence determination of equine relaxin.";
 RL Endocrinology 129:375-383(1991).
 CC -!- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN
 TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.
 CC -!- SUBUNIT: HETERO DIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
 DISULFIDE BONDS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 CC
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 CC
 CC EMBL; AB000201; BAA19069.1; -.
 CC EMBL; S78800; AAB35036.1; -.
 CC PIR; A49739; A49739.
 CC PIR; B49739; B49739.
 CC HSP; P01348; 4RLX.

RP SYNTHESIS.
 RX MEDLINE-91250367; PubMed-2040595;
 RA Buellbach E.E., Schwabe C.;
 RT "Total synthesis of human relaxin and human relaxin derivatives by
 solid-phase peptide synthesis and site-directed chain combination.";
 RL J. Biol. Chem. 266:10754-10761(1991).
 RN [5]
 RP PARTIAL SEQUENCE OF 25-51.
 RC TISSUE-Semen;
 RX MEDLINE-92241162; PubMed-1572287;
 RA Winslow J.W., Shih A., Bourell J.H., Weiss G., Reed B., Stults J.T.,
 RA Goldsmith L.T.;
 RT "Human seminal relaxin is a product of the same gene as human luteal
 relaxin";
 RL Endocrinology 130:2660-2668(1992).
 RN [6]
 RP SEQUENCE OF 25-53 AND 162-185.
 RX MEDLINE-91167739; PubMed-2076464;
 RA Winslow J.W., Griffin P.R., Rinderknecht E., Vandlen R.L.;
 RT "Structural characterization by mass spectrometry of native and
 recombinant human relaxin";
 RL Biomed. Environ. Mass Spectrom. 19:655-664(1990).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RX MEDLINE-92015205; PubMed-1656049;
 RA Eigenbrot C., Randal M., Quan C., Burnier J., O'Connell L.,
 RA Rinderknecht E., Kossiakoff A.A.;
 RT "X-ray structure of human relaxin at 1.5 A. Comparison to insulin and
 implications for receptor binding determinants";
 RL J. Mol. Biol. 221:15-21(1991).
 CC -1- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO
 PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS. MAY BE
 INVOLVED IN REMODELING OF CONNECTIVE TISSUES DURING PREGNANCY,
 PROMOTING GROWTH OF PUBIC LIGAMENTS AND RIPENING OF THE CERVIX.
 CC -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
 DISULFIDE BONDS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Expressed in the ovary during pregnancy. Also
 expressed in placenta, decidua and prostate.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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 DR EMBL; X00948; CAA25460.1; -;
 DR EMBL; AL135786; CAC04177.1; -;
 DR EMBL; AL135786; CAC04176.1; -;
 DR EMBL; S83200; AAD14429.1; -;
 DR EMBL; AL17315; CAA01324.1; -;
 DR EMBL; A06925; CAA00602.1; -;
 DR PIR; A60982; A60982;
 DR PDB; 6RLX; 31-OCT-93.
 DR MIM; 179740; -;
 DR InterPro; IPR000739; Insulin_IGF_relaxin.
 DR Pfam; PF00049; Insulin; 1.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Insulin family; Hormone; Multigene family; Signal; 3D-structure;
 KW Alternative splicing.
 FT SIGNAL 1 24
 FT CHAIN 25 53 RELAXIN B CHAIN.
 FT PROPEP 56 157 CONNECTING PEPTIDE.
 FT CHAIN 162 185 RELAXIN A CHAIN.
 FT MOD_RES 162 162 PYRROLIDONE CARBOXYLIC ACID.
 FT FT 162 162 INTERCHAIN.
 FT DISULFID 35 172 INTERCHAIN.
 FT DISULFID 47 185 INTERCHAIN.

FT DISULFID 171 176
 FT VARSPLIC 71 117
 FT FT
 FT VARSPLIC 118 185
 FT HELIX 27 29
 FT STRAND 31 32
 FT HELIX 36 49
 FT HELIX 163 173
 FT TURN 174 174
 FT STRAND 176 177
 FT HELIX 178 182
 FT TURN 183 184
 SQ SEQUENCE 185 AA; 21042 MW; AC73DBDE2090091B CRC64;

Query Match 14.4%; Score 109.5; DB 1; Length 185;
 Best Local Similarity 22.7%; Pred. No. 0.00084;
 Matches 42; Conservative 22; Mismatches 78; Indels 43; Gaps 4;
 QY 1 MARYMLLLAVVLTGELWPGAEARAAPYGVRLCGREFIRAVITFCGSRWRSDILAH 60
 Db 1 MPRLLFFHLLGVCLLNQFSRAVADSWMEVVKLCGRVRAQIAICGMSKSLSOE 60
 QY 61 EAMGDTFPDADADEDSLAGEAMGSSWLA-----LTKS-----PQ----- 98
 Db 61 DAQTPPVAIVPSPINKDTETINMMSEFVANLPQELKLTSEMOPALPOLQHQHPVLK 120
 QY 99 -----AFVGRPS-----WQGTGVLGRSDVLAGLSSSCCKWCCSKSE 137
 Db 121 DSSLLEEFKLLRNQSEADSSPSSELYLGLDTHSKKKQLYSALANKCHGVCTKRS 180
 QY 138 ISSLC 142
 Db 181 LARFC 185

RESULT 8
 ID REL2_PANTR STANDARD; PRT; 166 AA.
 AC P51455; P79267;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 GN Prolaxin H2 precursor (Fragment).
 OS RNL2 OR RLX2.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
 RC TISSUE=Placenta;
 RX MEDLINE-94238260; PubMed-8182365;
 RA Evans B.A., Fu P., Tregear G.W.;
 RT "Characterization of two relaxin genes in the chimpanzee.";
 RL J. Endocrinol. 140:385-392(1994).
 RN [2]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY.
 RC TISSUE=Placenta, and Ovary;
 RX MEDLINE-96328899; PubMed-8735594;
 RA Gunnarsen J.M., Fu P., Roche P.J., Tregear G.W.;
 RT "Expression of human relaxin genes: characterization of a novel
 alternatively-spliced human relaxin mRNA species.";
 RL Mol. Cell. Endocrinol. 118:85-94(1996).
 CC -1- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO
 PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS. MAY BE
 INVOLVED IN REMODELING OF CONNECTIVE TISSUES DURING PREGNANCY,
 PROMOTING GROWTH OF PUBIC LIGAMENTS AND RIPENING OF THE CERVIX.
 CC -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
 DISULFIDE BONDS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are

```

CC produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE CORPUS LUTEUM OF PREGNANCY
CC AND IN THE PLACENTA.
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z27245; CAA81758.1; -
CC DR EMBL; S83209; AAD14430.1; -
CC DR HSP; P04090; 6RLX.
CC DR InterPro; IPR000739; Insulin_IGF_relaxin.
CC DR Pfam; PF00049; Insulin; 1.
CC DR SMART; SM00078; ILGF; 1.
CC DR PROSITE; PS00262; INSULIN; 1.
CC KW Insulin family; Hormone; Multigene family; Signal; Polymorphism;
CC Alternative splicing.
CC FT NON_TER 1 5
CC FT SIGNAL <1 34
CC FT CHAIN 6 138
CC FT PROPEP 37 138
CC FT CHAIN 143 166
CC FT DISULFID 16 153
CC FT DISULFID 28 166
CC FT DISULFID 152 157
CC FT VARSPLIC 52 84
CC FT VARSPLIC 85 166
CC FT MISSING (IN ISOFORM 2).
CC FT VARIANT 30 34
CC FT KSTWS -> MSTLG (IN SOME ALLELES).
CC FT SEQUENCE 166 AA; 18760 MW; 220851E3134CEBDB CRC64;
CC -----
CC Query Match 14.3%; Score 108.5; DB 1; Length 166;
CC Best Local Similarity 23.4%; Pred. No. 0.00094;
CC Matches 36; Conservative 20; Mismatches 55; Indels 43; Gaps 4;
CC -----
CC QY 32 VRLGGRFIRAFVTCGSRWRSILAEAMGDTFPDADADESLAGELDAMSSWL 91
CC DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC 13 IKGLGRLVRAQIAICGKSTWSKLSQEDAPQTPRPAEIVPFSFINKDTETINMMSEFV 72
CC QY 92 A-----LTKS-----PQ-----AFYGRPS-----WQ 108
CC DB ANLPQELKLTLEMQPALPOLQYVPVVKDSLLFEEFKLIRNROSEADSPSELKYL 132
CC QY 109 GTPGVLRGSRDYLGLSSCCGKSCSEISLCL 142
CC DB 133 GLDTHSRKKRLYSALANKCHGVGCTKRLARFC 166
CC -----
CC RESULT 9
CC RELX_PIG
CC ID RELX_PIG STANDARD; PRT; 182 AA.
CC AC P01348;
CC DT 21-JUL-1986 (Rel. 01, Created)
CC DT 01-JUL-1989 (Rel. 11, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Prorelaxin precursor.
CC GN RIN.
CC OS Sus scrofa (Pig).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CC OX NCBI_TaxID=9823;
CC RN [1]
CC SEQUENCE FROM N.A.
CC RX MEDLINE=87308187; PubMed=2442155;
CC RA Haley J., Crawford R., Hudson P., Scanlon D., Tregear G., Shine J.,
CC Niall H.;

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RT Porcine relaxin. Gene structure and expression."
RL J. Biol. Chem. 262:11940-11946(1987).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=83157118; PubMed=6897721;
RA Haley J., Hudson P., Scanlon D., John M., Cronk M., Shine J.,
RA Tregear G., Niall H.;
RA "Porcine relaxin: molecular cloning and cDNA structure."
RL DNA 1:155-162(1982).
RN [3]
RN PRELIMINARY SEQUENCE OF 25-54 AND 161-182.
RX MEDLINE=77213067; PubMed=876374;
RA James R., Niall H., Kwok S., Bryant-Greenwood G.;
RA "Primary structure of porcine relaxin: homology with insulin and
RT related growth factors."
RL Nature 287:544-546(1977).
RN [4]
RN SEQUENCE OF 25-51.
RX MEDLINE=77157271; PubMed=851452;
RA Schwabe C., McDonald J.K., Steinetz B.G.;
RT "Primary structure of the B-chain of porcine relaxin."
RL Biochem. Biophys. Res. Commun. 75:503-510(1977).
RN [5]
RN SEQUENCE OF 25.
RX MEDLINE=77134136; PubMed=843375;
RA Schwabe C., McDonald J.K.;
RT "Demonstration of a pyroglutamyl residue at the N terminus of the B-
RL chain of porcine relaxin."
RT Biochem. Biophys. Res. Commun. 74:1501-1504(1977).
RN [6]
RN SEQUENCE OF 161-182.
RX MEDLINE=76231539; PubMed=938497;
RA Schwabe C., McDonald J.K., Steinetz B.G.;
RT "Primary structure of the A chain of porcine relaxin."
RL Biochem. Biophys. Res. Commun. 70:397-405(1976).
RN [7]
RN DISULFIDE BONDS.
RX MEDLINE=77236040; PubMed=887933;
RA Schwabe C., McDonald J.K.;
RT "Relaxin: a disulfide homology of insulin."
RL Science 197:914-915(1977).
RN [8]
RN 3D-STRUCTURE MODELING.
RX MEDLINE=78092399; PubMed=622170;
RA Isaacs N.W., James R., Niall H., Bryant-Greenwood G., Dodson G.G.,
RA Evans A., North A.C.T.;
RT "Relaxin and its structural relationship to insulin."
RL Nature 271:278-281(1978).
CC -!- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN
CC TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.
CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; K01088; AAA31114.1; -
CC DR EMBL; J02792; AAA31115.1; -
CC DR EMBL; A16593; CAA01295.1; -
CC DR EMBL; A06852; CAA00600.1; -
CC DR PIR; A01615; RXPG.
CC DR PIR; A29796; A29796.
CC DR PDB; 1RLX; 15-OCT-94.
CC DR PDB; 2RLX; 15-OCT-94.
CC DR PDB; 3RLX; 15-OCT-94.
CC DR PDB; 4RLX; 15-OCT-94.

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DR InterPro: IPR000739; Insulin_IGF_relaxin.
 DR Pfam: PF00049; Insulin_1.
 DR SMART: SM00078; ILGF_1.
 DR PROSITE: PS00262; INSULIN; 1.
 KW Insulin family; Hormone; Signal; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 56 RELAXIN B CHAIN.
 FT PROPEP 57 154 CONNECTING PEPTIDE.
 FT CHAIN 161 182 RELAXIN A CHAIN.
 FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 34 169 INTERCHAIN.
 FT DISULFID 46 182 INTERCHAIN.
 FT DISULFID 168 173
 FT CONFLICT 47 47
 FT CONFLICT 51 54 G -> GWMS (IN REF. 4).
 FT CONFLICT 116 116 WGR -> TWGR (IN REF. 3).
 FT CONFLICT 170 170 S -> L (IN REF. 1).
 FT CONFLICT 170 170 Q -> E (IN REF. 6).
 SQ SEQUENCE 182 AA; 20818 MW; 20736EB089F13AB4 CRC64;

Query Match 14.0%; Score 106.5; DB 1; Length 182;
 Best Local Similarity 21.7%; Pred. No. 0.0016;
 Matches 39; Conservative 22; Mismatches 68; Indels 51; Gaps 3;
 QY 9 LLVWVLTGEIWPAGAEARAAPYGVRLCGREFIRAVITCGGSRWRSDILAHEAMGDTFFP 68
 DB 8 LLGWLLLSQLPREIPQSTNDFTKACGRELVLWVEICGVSWSGTALSLEPQETGP 67
 QY 69 DADA-----DEDSLAGEIDAMSGSEWALTKSPQAFYGRPSWQ----- 108
 DB 68 PAETMPSSITKDAEILKMMLEFPNLPQELKATLSR-----QPSLRELQOSASKDSNLN 122
 QY 109 -----GTPGVLRGSRDVLGLSSCCCKWCGSKSEISSIC 142
 DB 123 FEFEKKIILNRQNEAEKSLLELKNLGLDKHSRKRFRMTLSEKCCQGVGCKIRKDARLC 182

RESULT 10
 INL3_BOVIN STANDARD; PRT; 132 AA.
 AC 077801;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
 GN INSL3 OR RLF.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Bathgate R.A.D., Balvers M., Hunt N., Ivell R.;
 RT "Relaxin-like factor gene is highly expressed in the bovine ovary of
 RT the cycle and pregnancy: sequence and messenger ribonucleic acid
 RT analysis.";
 RL Biol. Reprod. 55:1452-1457(1996).
 CC -!- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
 CC SPERMATOGENESIS.
 CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
 CC DISULFIDE BONDS (BY SIMILARITY).
 CC -!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN LEYDIG CELLS.
 CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 CC -----
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CC or send an email to license@isb-sib.ch.
 CC EMBL: AF094580; AACG3380.1;
 DR InterPro: IPR000739; Insulin_IGF_relaxin.
 DR Pfam: PF00049; Insulin; 1.
 DR SMART: SM00078; ILGF_1.
 DR PROSITE: PS00262; INSULIN; 1.
 KW Insulin family; Hormone; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 57 POTENTIAL.
 FT PROPEP 59 104 LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
 FT CHAIN 107 132 LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
 FT DISULFID 34 117 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 46 130 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 116 121 BY SIMILARITY.
 SQ SEQUENCE 132 AA; 14378 MW; A5585500C7F2241D CRC64;

Query Match 13.6%; Score 103.5; DB 1; Length 132;
 Best Local Similarity 28.5%; Pred. No. 0.0023;
 Matches 37; Conservative 17; Mismatches 43; Indels 33; Gaps 7;
 QY 23 AEAARAAPYGVRLCGREFIRAVITCGGSRWRSDILAHEAMGDTFFDADADS---LAG 79
 DB 24 AAQAEAP--EKLCGHHFVRALVRLCGPRWSSE-----DGRVAGDRELLRWLEG 73
 QY 80 E--LDEAMSGSE---WLALTKSPQA--FYGRPSWQGTGVLGRGSRDVLGLSSCCCKWG 132
 DB 74 QHLLGLGLMAGSDPVLVLAQPLPQASRRHHHRRATAINP-----ARHCCLSG 120
 QY 133 CSKSEISSIC 142
 DB 121 CTQODLLTLC 130

RESULT 11
 INL3_PIG STANDARD; PRT; 131 AA.
 AC P51461;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
 GN INSL3 OR RLF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Adham I.M., Burkhardt E., Benham M., Engel W.;
 RT "Cloning of a cDNA for a novel insulin-like peptide of the testicular
 RT Leydig cells.";
 RL J. Biol. Chem. 268:26668-26672(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Burkhardt E., Adham I.M., Brosig B., Gastmann A., Mattei M.-G.,
 RA Engel W.;
 RT "Structural organization of the porcine and human genes coding for a
 RT Leydig cell-specific insulin-like peptide (LEY I-L) and chromosomal
 RT localization of the human gene (INSL3).";
 RL Genomics 20:13-19(1994).
 CC -!- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
 CC SPERMATOGENESIS.
 CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
 CC DISULFIDE BONDS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN PRENATAL AND
 CC POSTNATAL LEYDIG CELLS.
 CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

--!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

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DR	EMBL; AJ011961;	CAA09888.1;	-.
DR	EMBL; AJ011962;	CAA09888.1;	JOINED.
DR	EMBL; AJ011961;	CAA09889.1;	-.
DR	HSSP; P01315;	IZEI.	
DR	InterPro; IPR000739;	Insulin_IGF_relaxin.	
DR	Pfam; PF00049;	Insulin; 1.	
DR	SMART; SM00078;	ILGF; 1.	
DR	PROSITE; PS02262;	INSULIN; 1.	
DR	Insulin family;	Hormone; Signal;	Alternative splicing.
FT	SIGNAL	1	24
FT	CHAIN	25	55
FT	PROPEP	58	104
FT	CHAIN	107	131
FT	DISULFID	34	117
FT	DISULFID	46	130

[illegible]

QY	142 C 142
Db	130 C 130
RESULT 13	
RELX_MACMU	
ID	STANDARD; PRT; 185 AA.
AC	P19884;
DT	01-FEB-1991 (Rel. 17, Created)
DT	01-FEB-1991 (Rel. 17, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	prorelaxin precursor.
GN	RLN.
OS	Macaca mulatta (Rhesus macaque).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC	Cercopithecinae; Macaca.
OX	NCBI_TaxID=9544;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=90073957; PubMed=2590381;
RA	Crawford R.J., Hammond V.E., Roche P.J., Johnston P.D., Tregear G.W. ;
RT	"structure of rhesus monkey relaxin predicted by analysis of the single-copy rhesus monkey relaxin gene.";
RT	J. Mol. Endocrinol. 3:169-174(1989).
RL	-I- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS. MAY BE INVOLVED IN REMODELING OF CONNECTIVE TISSUES DURING PREGNANCY,
CC	

PROMOTING GROWTH OF PUBIC LIGAMENTS AND RIPENING OF THE CERVIX.
 CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
 CC DISULFIDE BONDS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 DR PIR; A34936; A34936.
 DR HSSP; P04090; 6RLX.
 DR InterPro; IPR000739; Insulin_IGF_relaxin.
 DR Pfam; PF00049; Insulin; 1.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Insulin family; Hormone; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 53 RELAXIN B CHAIN (PROBABLE).
 FT PROPEP 56 157 CONNECTING PEPTIDE (PROBABLE).
 FT CHAIN 161 185 RELAXIN A CHAIN (PROBABLE).
 FT DISULFID 35 172 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 47 185 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 171 176 BY SIMILARITY.
 SQ SEQUENCE 185 AA; 20895 MW; 7E3C5D21B57E185C CRC64;

Query Match 13.4%; Score 101.5; DB 1; Length 185;
 Best Local Similarity 22.7%; Pred. No. 0.0051;
 Matches 42; Conservative 22; Mismatches 78; Indels 43; Gaps 4;

QY 1 MARYMLLLIAVWVLTGELWPGAEARAAPYVRLCGREFIRAVFTCGGSRWRSDILAH 60
 Db 1 MPRLEFLHLLGCLLNQFSAVAKWMDVVKACGRELVAQIAICGKSTLGKSLNQE 60
 QY 61 EAMGDTFFPADADESLAGELDEAMGSEWLA-----LTKSP----- 97
 Db 61 DAPLKPRAAEIVPSLINQDTETINMSEFVANPLQELKLTLSERQPALSELQHHVPVLK 120
 QY 98 -----QAFYRGPRPS-WQGTGVLRG-----SRDVLGSLSSCKKWCSE 137
 Db 121 DSNLSFEFPKRIIRKQSEATSSSELSGLDTHSRKRYLTWLSNKKCHIGCTKRS 180
 QY 138 ISSLC 142
 Db 181 LAKFC 185

RESULT 14
 ID RELX_RAJER STANDARD; PRT; 64 AA.
 AC P11952;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Relaxin.
 OS Raja erinacea (Little skate).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squala; Hymnosqualea; Pristiogaster; Batoidae;
 OC Rajiformes; Rajidae; Raja.
 OX NCBI_TaxID=7782;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Ovary;
 RX MEDLINE=87156758; PubMed=3827922;
 RA Bullebach E.B., Schwabe C., Callard I.P.;
 RT "Relaxin from an oviparous species, the skate (Raja erinacea).";
 RL Biochem. Biophys. Res. Commun. 143:273-280(1987).
 CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
 CC DISULFIDE BONDS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 DR PIR; A29543; A29543.
 DR HSSP; P04090; 6RLX.
 DR InterPro; IPR000739; Insulin_IGF_relaxin.
 DR Pfam; PF00049; Insulin; 1.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.

KW Insulin family; Hormone.
 FT CHAIN 1 40 RELAXIN B CHAIN.
 FT NON_CONS 40 41
 FT CHAIN 41 64 RELAXIN A CHAIN.
 FT DISULFID 11 51 INTERCHAIN.
 FT DISULFID 23 64
 FT DISULFID 50 55
 SQ SEQUENCE 64 AA; 7499 MW; E7AC62B8BA81F49D CRC64;

Query Match 13.2%; Score 100.5; DB 1; Length 64;
 Best Local Similarity 22.1%; Pred. No. 0.002;
 Matches 27; Conservative 11; Mismatches 25; Indels 59; Gaps 3;

QY 21 PGARARAAPYVRLCGREFIRAVFTCGGSRWRSDILAHAMGDTFFDADADESLAGE 80
 Db 2 PNWEERS-----RLCGRLIRAFIYLCGTRWLPNFGNYPI----- 39
 QY 81 LDEAMGSEWLAATKSPQAFYRGPRPSWQGTGVLGRSDVLGLSSCKKWCSEISS 140
 Db 40 MEKMW-----GFAKKCAIGCSTEDFRM 62

QY 141 LC 142
 Db 63 VC 64

RESULT 15

ID INL3_RAT STANDARD; PRT; 105 AA.
 AC Q9WUK0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Leydig insulin-like peptide (Ley-I-L) (Relaxin-like factor) (Fragment).
 DE INSL3 OR RLF.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA Spless A.-N., Pusch W., Ivell R.;
 RT "Cloning and sequence of the rat relaxin-like factor and its promoter.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND SPERMATOGENESIS.
 CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
 CC DISULFIDE BONDS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN LEYDIG CELLS.
 CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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 CC
 DR EMBL; AF139918; AAD33663.1;
 DR InterPro; IPR000739; Insulin_IGF_relaxin.
 DR Pfam; PF00049; Insulin; 1.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Insulin family; Hormone.
 FT CHAIN 1 1
 FT NON_TER <1 1
 FT CHAIN ? 77
 FT PROPEP ? 77
 LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
 C PEPTIDE (POTENTIAL).


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Query Match      100.0%; Score 132; DB 22; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 24: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match 47.7%; Score 63; DB 19; Length 135;
Best Local Similarity 52.6%; Pred. No. 0.88;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 6 LSSCCKWGCSKSEISLC 24
| : ||: ||| | : | : ||

Db 117 lqalcrcgcmkclstlc 135

RESULT

AA95771 3

ID AAY95771 standard; Protein; 135 AA.

AC AAY95771;

DT 07-NOV-2000 (first entry)

DE Mouse insulin family homologue zins3.

KW Zins3; insulin; relaxin; mouse; NIDDM;

XX non-insulin dependent diabetes mellitus; diagnosis.

OS Mus musculus.

XX WO200047776-A2.

PN 17-AUG-2000.

PD 10-FEB-2000; 2000WO-US03515.

PF 12-FEB-1999; 99US-0198248.

PR 12-FEB-1999; 99US-0250125.

XX (ZYMO) ZYMOGENETICS INC.

PA Jaspers SR, Whitmore TE, Conklin DC, Lofton-Day CE, Lok S;

PI WPI; 2000-558220/51.

DR N-PSDB; AAA50153.

XX Identifying mutations in human chromosome 1p31, preferably a zins3 gene

PT mutation, comprises using an insulin/relaxin family member (designated

PT zins3), useful for diagnosing non-insulin dependent diabetes

XX Example 4; Page 46-47; 51pp; English.

CC The present sequence is that of a murine paralog (see AAY95771) of

CC human zins3 (see AAY95770), a novel member of the insulin/relaxin

CC family member that maps to a region of human chromosome 1 associated

CC with non-insulin dependent diabetes mellitus (NIDDM). The sequence

CC was deduced from an isolated cDNA clone (see AAA50153). Northern

CC blots of embryo tissue indicated that mouse zins3 is expressed in

CC a developmentally regulated fashion. zins3 polynucleotides and

CC polypeptides can be used to diagnose disorders associated with

CC abnormal expression of zins3, and to identify polymorphisms that

CC result from mutations in the human zins3 gene. The invention

CC provides methods for identifying abnormalities in expression that

CC are a factor in causing, or predisposing, a person to some defect

CC in glucose metabolism, such as NIDDM.

XX Sequence 135 AA;

Query Match

Best Local Similarity 47.7%; Score 63; DB 21; Length 135;

Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCKSKSEISL 24

Db 117 lqalcrcgcmkclstlc 135

XX

DE

XX

KW

XX

OS

XX

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FT

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FT

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XX

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XX

FT

XX

FT

Human relaxin-related factor-1 (RRF-1).

Relaxin-related factor-1; RRF-1; testis; sperm; growth factor; infertility.

Homo sapiens.

Key

Location/Qualifiers

1-29

/label- Sig_peptide

Misc-difference 178

/note= "conserved Cys residue indicative of insulin family member"

Misc-difference 179

/note= "conserved Cys residue indicative of insulin family member"

Misc-difference 183

/note= "conserved Cys residue indicative of insulin family member"

Misc-difference 192

/note= "conserved Cys residue indicative of insulin family member"

WO9716549-A2.

09-MAY-1997.

01-NOV-1996; 96WO-US17342.

21-FEB-1996; 96US-0012016.

03-NOV-1995; 95US-0006221.

(REGE-) REGENERON PHARM INC.

Davis S;

WPI; 1997-272118/24.

N-PSDB; AAT68418.

New isolated relaxin-related factor genes - used to develop products which can be used in diagnosis and therapy, e.g. in fertility and pregnancy applications

Example 1; Fig 1; 34pp; English.

Human relaxin-related factor-1 (RRF-1) (AAW17675) is a testis-specific growth factor related to relaxin and to the insulin family of ligands. RRF-1 cDNA (AAW68418) was isolated in a search of expressed sequence tags for sequences related to relaxin. RRF-1 displays all the expected features of a new insulin family member, partic. with regard to a cluster of four cysteine residues at the C-terminus of the molecule. A related placenta-specific factor, RRF-2 (AAW17676), has also been identified. RRF-1 can be produced in transformed host cells for use in the prepn. of antibodies and therapeutic compns., or as a growth factor for maintaining cells in culture. RRF-1 may be involved in the maturation of sperm and may have a role in treatment of fertility disorders.

Sequence 213 AA;

Query Match 46.2%; Score 61; DB 18; Length 213;

Best Local Similarity 50.0%; Pred. No. 2.4;

Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 5 GLSSCKCKWGCKSKSEISL 24

Db 173 gysekcltgcctkeelsiac 192

RESULT 5

AAW47548

us-09-781-077-2_copy_119_142.rag

Fri Jun 28 11:32:03 2002

```

ID AAW47548 standard; Protein; 213 AA.
XX AC
XX AAW47548;
XX DT
XX 03-JUL-1998 (first entry)
XX DE
XX Human Zins2 testis-specific insulin homologue.
XX KW
XX Human; Zins2; testis-specific insulin homologue; differentiation;
KW cryopreserved sperm viability; sperm motility; proliferation;
KW egg/sperm interaction; fertilisation; testicular cell; vaccine;
KW immunocontraception; contraception; in vitro fertilisation.
XX OS
XX Homo sapiens.
XX PN
XX WO9805782-Al.
XX PD
XX 12-FEB-1998.
XX PF
XX 01-AUG-1997; 97WO-US13879.
XX PR
XX 21-NOV-1996; 96US-0031592.
XX PR
XX 02-AUG-1996; 96US-0023213.
XX PA
XX (ZYMO ) ZYMOGENETICS INC.
XX XX
XX Adams RL, Conklin DC, Jaspers SR, Jelmborg AC, Lofton-Day CE;
PI Lok S;
XX DR
XX WPI; 1998-145618/13.
XX DR
XX N-PSDB; AAV18663.
XX XX
XX Testis-specific insulin homologue poly:peptide(s) - may be used,
PT e.g. in enhancing viability of cryo:preserved sperm, enhancing sperm
PT motility or in immuno:contraception methods
XX PS
XX Claim 10; Pages 73-74; 91pp; English.
XX XX
XX The present sequence is human Zins2 testis-specific insulin
CC homologue, which may be used to enhance the viability of
CC cryopreserved sperm, sperm motility, egg/sperm interactions,
CC fertilisation or proliferation or differentiation of testicular
CC cells. Zins2 may also be used as a vaccine, e.g. in
CC immunocontraception methods to prevent fertilisation. Antagonists,
CC e.g. anti-Zins2 binding protein, may be used in contraception.
CC Zins2 is especially useful for in vitro fertilisation methods.
XX SQ
XX Sequence 213 AA;

Query Match 46.2%; Score 61; DB 19; Length 213;
Best Local Similarity 50.0%; Pred. No. 2.4;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 5 GLSSCCCKWGCKSEISLSC 24
| | | | | | | |
DB 173 gysekccitgtckeelsiac 192

RESULT 6
AAW47547
ID AAW47547 standard; Protein; 188 AA.
XX AC
XX AAW47547;
XX DT
XX 03-JUL-1998 (first entry)
XX DE
XX Rat Zins2 testis-specific insulin homologue.
XX KW
XX Rat; Zins2; testis-specific insulin homologue; differentiation;
KW cryopreserved sperm viability; sperm motility; proliferation;
KW egg/sperm interaction; fertilisation; testicular cell; vaccine;
KW immunocontraception; contraception; in vitro fertilisation.

```

```

XX Rattus rattus.
XX OS
XX WO9805782-Al.
XX PN
XX 12-FEB-1998.
XX PD
XX 01-AUG-1997; 97WO-US13879.
XX PF
XX 21-NOV-1996; 96US-0031592.
XX PR
XX 02-AUG-1996; 96US-0023213.
XX PA
XX (ZYMO ) ZYMOGENETICS INC.
XX XX
XX Adams RL, Conklin DC, Jaspers SR, Jelmborg AC, Lofton-Day CE;
PI Lok S;
XX DR
XX WPI; 1998-145618/13.
XX DR
XX N-PSDB; AAV18662.
XX XX
XX Testis-specific insulin homologue poly:peptide(s) - may be used,
PT e.g. in enhancing viability of cryo:preserved sperm, enhancing sperm
PT motility or in immuno:contraception methods
XX PS
XX Claim 8; Pages 66-67; 91pp; English.
XX XX
XX The present sequence is rat Zins2 testis-specific insulin
CC homologue, which may be used to enhance the viability of
CC cryopreserved sperm, sperm motility, egg/sperm interactions,
CC fertilisation or proliferation or differentiation of testicular
CC cells. Zins2 may also be used as a vaccine, e.g. in
CC immunocontraception methods to prevent fertilisation. Antagonists,
CC e.g. anti-Zins2 binding protein, may be used in contraception.
CC Zins2 is especially useful for in vitro fertilisation methods.
XX SQ
XX Sequence 188 AA;

Query Match 44.7%; Score 59; DB 19; Length 188;
Best Local Similarity 45.0%; Pred. No. 3.8;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 5 GLSSCCCKWGCKSEISLSC 24
| | | | | | | |
DB 163 gfadkccaigcskeelavac 182

RESULT 7
AAP30192
ID AAP30192 standard; Protein; 22 AA.
XX AC
XX AAP30192;
XX DT
XX 03-AUG-1992 (first entry)
XX DE
XX Sequence encoded by synthetic gene for porcine relaxin A chain.
XX KW
XX Hormone; labour; pregnancy; parturition; control; induction.
XX OS
XX Pig.
XX PN
XX EP68375-A.
XX PD
XX 05-JAN-1983.
XX PF
XX 19-JUN-1982; 82EP-0105405.
XX PR
XX 22-JUN-1981; 81GB-0019138.
XX PA
XX (SEAR ) SEARLE G D & CO.
XX PI
XX Stewart AG, Bell LD;
XX XX

```

DR WPI; 1983-04897K/03.
 XX N-PSDB; AAN30124.
 PT Prodn. of porcine relaxin from synthetic genes - useful for
 PT induction and control of labour in women
 XX Disclosure; Fig 1; 38pp; English.
 PS
 XX The inventors claim synthetic genes for porcine relaxin. The genes
 CC may contain, in addn. to the coding sequence, a stop codon, an
 CC initiator methionine codon, restriction sites for Cla I and Bam HI
 CC etc. Porcine relaxin is useful in the induction and control of
 CC labour in women. In sows admin. during farrowing may reduce the
 CC rate of still birth of piglets.
 XX
 SQ Sequence 22 AA;
 Query Match 43.9%; Score 58; DB 4; Length 22;
 Best Local Similarity 47.4%; Pred. No. 0.74;
 Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 6 LSSSCCKGCGSKSEISL 24
 II II: II: II: II:
 Db 4 lsekccqvcirkdiaric 22
 RESULT 8
 AAP30392
 ID AAP30392 standard; Protein; 182 AA.
 XX
 AC AAP30392;
 XX
 DT 25-MAY-1992 (first entry)
 XX
 DE Sequence of porcine preprorelaxin.
 XX
 KW Relaxin; hormone.
 XX
 OS Sus scrofa domestica.
 XX
 PN EP86649-A.
 XX
 PD 24-AUG-1983.
 XX
 PF 12-FEB-1983; 83EP-0021967.
 XX
 PR 12-FEB-1982; 82AU-0002695.
 PR 11-FEB-1983; 83AU-0011834.
 XX
 PA (FLOR-) FLOREY INST EXP PHY.
 PA (HOWA-) HOWARD FLOREY INST.
 XX
 PI Hudson PJ, Haley JD, Niall HD, Shine J;
 XX
 DR WPI; 1983-748587/35.
 DR N-PSDB; AAN30196.
 XX
 XX Genes and DNA transfer vectors for prorelaxin expression - useful
 in prodn. of porcine relaxin for veterinary and human use
 PT Disclosure; Fig 5; 50pp; English.
 PS
 XX The inventors claim synthetic porcine preprorelaxin and prorelaxin
 CC and synthetic A, B and C peptide chains of prolaxin, and a gene for
 CC expression of porcine preprorelaxin or prorelaxin, and their sub-
 CC units (see AAN30186). They also claim a double-stranded DNA fragment
 CC for the expression of the signal peptide chain of porcine
 CC preprorelaxin comprising a coding strand and a complementary strand
 CC corresp. to a defined mRNA sequence (see AAN30187-N30194) which
 CC corresp. to the most homologous regions between the pig and rat cDNA
 CC sequences. A probe (AAN30195) is also claimed.
 XX

SQ Sequence 182 AA;

Query Match 43.9%; Score 58; DB 4; Length 182;
 Best Local Similarity 47.4%; Pred. No. 5;
 Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 LSSSCCKGCGSKSEISL 24
 II II: II: II: II:
 Db 164 lsekccqvcirkdiaric 182

RESULT 9

AAP40156
 ID AAP40156 standard; Protein; 182 AA.
 XX

AC AAP40156;

XX
 DT 11-FEB-1992 (first entry)
 XX

DE Sequence of porcine preprorelaxin.

XX Labour; birth; hormone; relaxin.

XX OS Fig.

XX Key Location/Qualifiers

FT Peptide 1..25

FT Peptide /label= signal

FT Peptide 26..57

FT Peptide /label= B-chain

FT Peptide 58..160

FT Peptide /label= C-peptide

FT Peptide 161..182

FT Peptide /label= A-chain

XX EP101309-A.

XX 22-FEB-1984.

XX PD

XX PF 11-AUG-1983; 83EP-0304662.

XX PR 12-AUG-1982; 82AU-0005352.

XX PR 11-AUG-1983; 83AU-0017906.

XX PR 01-JAN-1988; 88EP-0104503.

XX PA (FLOR-) HOWARD FLOREY INST.

XX PA (HOWA-) HOWARD FLOREY INST.

XX Hudson PJ, Shine J, Niall HD, Tregear GW;

XX WPI; 1984-050918/09.

XX DR N-PSDB; AAN40125, AAN40126.

XX XX

PT Genes for human relaxin, prorelaxin and preprorelaxin prodn. -
 prepd. by recombinant DNA techniques

XX Disclosure; Fig 3; 51pp; English.

XX PS

XX CC The inventors claim the gene for the expression of human

XX CC preprorelaxin (HPP) and its sub-units. Also claimed are synthetic

XX CC HPP, HP, fragments and analogues. Human relaxin and its analogues

XX CC are prepd. for therapeutic purposes, esp. in clinical intervention

XX CC in cases of difficult labour.

XX SQ Sequence 182 AA;

Query Match

Best Local Similarity 43.9%; Score 58; DB 5; Length 182;

Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 LSSSCCKGCGSKSEISL 24

Db 164 lsekccqvcirkdiarlc 182

RESULT 10
AA01962
ID AAY01962 standard; Peptide; 27 AA.

XX AC AAY01962;
XX DT 01-JUL-1999 (first entry)
XX DE Insulin-like peptide (pro-ILP) chain A peptide.
XX KW Insulin-like polypeptide; pro-ILP; ILP; insulin/IGF family;
XX KW A chain; B chain; C chain; neurophysiological function;
XX KW fluid homeostasis; electrolyte homeostasis; cardiovascular function;
XX KW blood pressure; somatic; cardiac ionotropic activity;
XX KW cardiac chronotropic activity; collagen deposition.

XX OS Homo sapiens.
XX PN WO9915664-A1.
XX PD 01-APR-1999.
XX PF 28-AUG-1998; 98WO-US17888.
XX PR 24-SEP-1997; 97US-0059836.
XX PA (GETH) GENENTECH INC.

XX PI Gurney A;
XX DR WPI; 1999-254713/21.
XX DR N-PSDB; AAX35209.
XX PT Colon and uterus expressed insulin-like polypeptide, useful in the
XX PT treatment of disorders related to neurophysiological function
XX PS Claim 7; Page -; 75pp; English.

XX CC The present sequence represents insulin-like polypeptide (pro-ILP)
XX CC chain A peptide. The ILP protein is expressed in the colon and uterus,
XX CC and is a member of the insulin/IGF family. The immature pro-ILP
XX CC comprises a 135 amino acid sequence, which is processed into the mature
XX CC form which comprises an A chain and a B chain linked by disulfide bonds.
XX CC The C-peptide of pro-ILP exists as a separate peptide after processing
XX CC of pro-ILP. The ILP protein is useful in treatment of disorders related
XX CC to neurophysiological function affecting fluid homeostasis, electrolyte
XX CC homeostasis, cardiovascular function, blood pressure, somatic or cardiac
XX CC ionotropic activity, cardiac chronotropic activity and collagen
XX CC deposition. The methods can be used for diagnosing a physiologic or
XX CC pathologic condition of the uterus, colon or other ILP-expressing cell
XX CC or tissue and for diagnosis and screening of modulators and therapeutics.
XX CC note: the present sequence does not appear in the specification; it was
XX CC created using information provided.

XX SQ Sequence 27 AA;

Query Match 43.2%; Score 57; DB 20; Length 27;
Best Local Similarity 47.4%; Pred. No. 1.2;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCKSKSEISLCL 24
| : || ||| :||| :|||
Db 9 lqtictdgcsmtdisalc 27

RESULT 11
AAW37925
ID AAW37925 standard; Protein; 135 AA.

XX AAW37925;
XX DT 01-SEP-1998 (first entry)
XX DE Human Zins3 protein.
XX KW Insulin homologue; identification; isolation; Zins3 receptor;
XX KW treatment; disease; pre-eclampsia; premature labour; Human.

XX OS Homo sapiens.
XX FH Key
XX FT Peptide Location/Qualifiers
XX FT /note= "B chain"
XX FT Peptide 23..48
XX FT /note= "C-peptide"
XX FT Peptide 49..114
XX FT 115..135
XX FT /note= "A chain"

XX PN WO9816635-A1.
XX PD 23-APR-1998.
XX PF 15-OCT-1997; 97WO-US18593.
XX PR 15-OCT-1996; 96US-0028177.
XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Conklin DC, Jaspers SR, Lofton-Day CE, Lok S;
XX DR WPI; 1998-251285/22.
XX DR N-PSDB; AAV29150.
XX PT Insulin homologue polypeptide(s) and antagonists - used to, e.g.
XX PT treat pre-eclampsia, premature labour and Crohn's disease
XX PS Claim 2; Page 64-65; 81pp; English.

XX CC The Zins3 protein is an insulin homologue protein. Polynucleotide
XX CC molecules taken from its gene can be introduced into a cultured cell
XX CC using an expression vector. The cell will express an insulin homologue
XX CC polypeptide encoded by the polynucleotide. The polypeptides can also be
XX CC expressed by introducing the polynucleotides into the germline of a
XX CC nonhuman animal. The polypeptides can be used to identify and isolate
XX CC receptors for Zins3. Antibodies and antagonists of the polypeptides can
XX CC be used for treating disease associated with extracellular matrix and
XX CC vessels. The antibodies may also be used in the diagnosis of diseases
XX CC associated with the polypeptide, such as reproductive disorders
XX CC associated with the placenta and uterus, gastrointestinal diseases, and
XX CC placental and colon pathology. Antagonists against the polypeptide may
XX CC also be used to treat diseases such as preclampsia, premature labour, and
XX CC Crohn's disease.

XX SQ Sequence 135 AA;

Query Match 43.2%; Score 57; DB 19; Length 135;
Best Local Similarity 47.4%; Pred. No. 5.1;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCKSKSEISLCL 24
| : || ||| :||| :|||
Db 117 lqtictdgcsmtdisalc 135

RESULT 12
AAW01961
ID AAY01961 standard; Protein; 135 AA.

XX AC AAY01961;
XX AC AAY01961;

DT	01-JUL-1999	(first entry)	
DE	Pro-insulin-like peptide (pro-ILP).		
KW	Insulin-like polypeptide; pro-ILP; ILP; insulin/IGF family;		
KW	A chain; B chain; C chain; neurophysiological function;		
KW	fluid homeostasis; electrolyte homeostasis; cardiovascular function;		
KW	blood pressure; somatic; cardiac inotropic activity;		
KW	cardiac chronotropic activity; collagen deposition.		
OS	Homo sapiens.		
XX	WO9915664-A1.		
PN	01-APR-1999.		
PD	28-AUG-1998; 98WO-US17888.		
PF	24-SEP-1997; 97US-0059836.		
PR	(GETH) GENENTECH INC.		
XX	Gurney A;		
PI	WPI; 1999-254713/21.		
XX	N-PSDB; AAX35204.		
DR	Colon and uterus expressed insulin-like polypeptide, useful in the		
PT	treatment of disorders related to neurophysiological function		
PS	Claim 5; Fig 6B; 75pp; English.		
XX	The present sequence represents an insulin-like polypeptide' (pro-ILP).		
CC	The protein is expressed in the colon and uterus and is a member		
CC	of the insulin/IGF family. The immature pro-ILP comprises a 135 amino		
CC	acid sequence, which is processed into the mature form which comprises		
CC	an A chain and a B chain linked by disulfide bonds. The C-peptide of		
CC	pro-ILP exists as a separate peptide after processing of pro-ILP. The		
CC	ILP protein is useful in treatment of disorders related to		
CC	neurophysiological function affecting fluid homeostasis, electrolyte		
CC	homeostasis, cardiovascular function, blood pressure, somatic or cardiac		
CC	inotropic activity, cardiac chronotropic activity and collagen		
CC	deposition. The methods can be used for diagnosing a physiologic or		
CC	pathologic condition of the uterus, colon or other ILP-expressing cell		
CC	or tissue and for diagnosis and screening of modulators and therapeutics.		
XX			
SQ	Sequence 135 AA;		
	Query Match 43.2%; Score 57; DB 20; Length 135;		
	Best Local Similarity 47.4%; Pred. No. 5.1;		
	Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;		
QY	6 LSSSCCKGCKSEISLSC 24		
	: ::		
Db	117 lgtlctdgcsmtdlsalc 135		
RESULT 13			
AAB00173			
ID	AAB00173 standard; Protein; 135 AA.		
XX			
AC	AAB00173;		
DT	08-FEB-2001 (first entry)		
XX			
DE	PRO182 polypeptide.		
XX			
PRO211; PRO228; PRO538; PRO172; PRO182; neoplasia; inhibition;			
tumour; treatment; therapy; agonist; antibody; breast cancer;			
ovarian cancer; renal cancer; colorectal cancer; uterine cancer;			
prostate cancer; lung cancer; bladder cancer; melanoma; leukaemia;			
inflammatory disorder; angiogenic disorder; immunologic disorder;			

CC nucleic acids and the proteins they encode may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors
CC containing them and the PRO polypeptide may be used to treat disorders
CC associated with decreased PRO expression. AAA77510 to AAA77721 and
CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in
CC the exemplification of the present invention.

XX
SQ Sequence 135 AA;

Query Match 43.2%; Score 57; DB 21; Length 135;
Best Local Similarity 47.4%; Pred. No. 5.1;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 6 LSSSCCKWGCSEISLSC 24
| : || ||| :|||
Db 117 lqtlcctdgcsmtdlsalc 135

RESULT 15
AAB24391
ID AAB24391 standard; Protein: 135 AA.
XX
AC AAB24391;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human insulin family homologue zins3.
XX
KW Zins3; insulin; relaxin; human; diagnosis; NIIDM;
KW non-insulin dependent diabetes mellitus.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide /label= Signal_peptide
FT Peptide /label= B-chain
FT Peptide /label= C-chain
FT Peptide /label= A-chain
FT Peptide /label= A-chain
XX WO200047776-A2.
XX PN 17-AUG-2000.
XX PD 10-FEB-2000; 2000WO-US03515.
XX PF 12-FEB-1999; 99US-0198248.
XX PR 12-FEB-1999; 99US-0250125.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX Jaspers SR, Whitmore TE, Conklin DC, Lofton-Day CE, Lok S;
XX WPI: 2000-558220/51.
XX N-PSDB; AAA50150.
XX
XX Identifying mutations in human chromosome 1p31, preferably a zins3 gene
XX mutation, comprises using an insulin/relaxin family member (designated
XX zins3), useful for diagnosing non-insulin dependent diabetes -
XX
XX Claim 2; Page 44-45; 51pp; English.
XX
XX The present sequence is that of zins3, a novel member of the
XX insulin/relaxin family. The zins3 gene maps to human chromosome
XX 1p31, a region that is correlated to a heritable form of non-insulin
XX dependent diabetes mellitus (NIIDM). zins3 mRNA is not expressed

CC nucleic acids and the proteins they encode may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors
CC containing them and the PRO polypeptide may be used to treat disorders
CC associated with decreased PRO expression. AAA77510 to AAA77721 and
CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in
CC the exemplification of the present invention.

XX
SQ Sequence 135 AA;

Query Match 43.2%; Score 57; DB 21; Length 135;
Best Local Similarity 47.4%; Pred. No. 5.1;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 6 LSSSCCKWGCSEISLSC 24
| : || ||| :|||
Db 117 lqtlcctdgcsmtdlsalc 135

RESULT 14
AAB24391
ID AAB24391 standard; Protein: 135 AA.
XX
AC AAB24391;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human PRO182 protein sequence SEQ ID NO:16.
XX
KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
KW cytostatic; gene therapy; vaccine.
XX
XX Homo sapiens.
XX
XX WO200032221-A2.
XX
XX PD 08-JUN-2000.
XX
XX PF 30-NOV-1999; 99WO-US28313.
XX
XX PR 01-DEC-1998; 98WO-US25108.
XX PR 16-DEC-1998; 98US-0112850.
XX PR 12-JAN-1999; 99US-0115554.
XX PR 08-MAR-1999; 99WO-US05028.
XX PR 12-MAR-1999; 99US-0123957.
XX PR 28-APR-1999; 99US-0131445.
XX PR 14-MAY-1999; 99US-0134287.
XX PR 02-JUN-1999; 99WO-US12252.
XX PR 23-JUN-1999; 99US-0141037.
XX PR 20-JUL-1999; 99US-0144758.
XX PR 26-JUL-1999; 99US-0145698.
XX PR 01-SEP-1999; 99WO-US20111.
XX PR 08-SEP-1999; 99WO-US20594.
XX PR 13-SEP-1999; 99WO-US20944.
XX PR 15-SEP-1999; 99WO-US21090.
XX PR 05-OCT-1999; 99WO-US21547.
XX PR 29-OCT-1999; 99WO-US23089.
XX PR 29-OCT-1999; 99US-0162506.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
XX Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
XX Watanabe CK, Williams PM, Wood WI;
XX
XX WPI: 2000-412154/35.
XX N-PSDB; AAA77521.
XX
XX Nucleic acids encoding PRO polypeptides useful for preventing,
XX diagnosing and treating diabetes a cardiovascular, endothelial or
XX angiogenic disorders in mammals -
XX
XX Claim 72; Fig 8; 315pp; English.
XX
XX The present invention describes nucleic acids encoding PRO polypeptides
XX useful for preventing, diagnosing and treating diabetes a
XX cardiovascular, endothelial or angiogenic disorder in mammals by
XX modulating cell proliferation, angiogenesis and cardiovascularisation,
XX and for identifying agonists and antagonists of these processes. The

CC in detectable amounts in healthy tissue, indicating that the zins3
CC polynucleotide is a candidate marker for a disease state and/or a
CC specialized cell type. zins3 polynucleotides and polypeptides can
CC be used to diagnose disorders associated with abnormal expression
CC of the zins3 protein, and to identify polymorphisms that result
CC from mutations in the zins3 gene. In particular, the invention
CC provides methods for identifying abnormalities in expression that
CC are a factor in causing, or predisposing, a person to some defect
CC in glucose metabolism, such as NIDDM. Processing of the mature
CC zins3 protein involves cleavage at the C-terminus of the signal
CC peptide and, based on predicted structural homology with other
CC members of the insulin family, cleavage at the C-terminus of the
CC B-chain and at the N-terminus of the A-chain, resulting in
CC removal of the C-peptide. Cysteine residues at positions 29 and 41
CC (B-chain) and 121 and 135 (A-chain) are capable of associating
CC through cysteine bridges and forming disulfide-bonded molecules.
XX

SQ Sequence 135 AA;

Query Match 43.2%; Score 57; DB 21; Length 135;
Best Local Similarity 47.4%; Pred. No. 5.1;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 6 LSSCKKGGCKSKSEISLC 24
| : || ||| :|||
Db 117 lqtclctdgcsmtdlsalc 135

Search completed: June 27, 2002, 16:08:09
Job time: 278 sec

1. The first part of the document is a list of the names of the persons who were present at the meeting. The names are listed in alphabetical order.

Result No.	Score	Query Match	Length	DB	ID	Description
1	74	56.1	24	6	5464756-8	Patent No. 5464756
2	63	47.7	24	6	5464756-7	Patent No. 5464756
3	63	47.7	135	3	US-08-950-720A-6	Sequence 6, Appl
4	61	46.2	213	4	US-08-905-267-13	Sequence 13, Appl
5	61	46.2	213	4	US-09-314-051-13	Sequence 13, Appl
6	59	44.7	188	2	US-08-905-267-2	Sequence 2, Appl
7	59	44.7	188	4	US-08-905-267-2	Sequence 2, Appl
8	58	43.9	22	6	US-09-314-051-2	Patent No. 5464756
9	57	43.2	24	6	5464756-4	Patent No. 5464756
10	57	43.2	135	3	US-08-950-720A-2	Sequence 2, Appl
11	57	43.2	928	1	US-08-442-248-2	Sequence 2, Appl
12	57	43.2	928	1	US-08-440-815-2	Sequence 2, Appl
13	57	43.2	928	4	US-08-486-449-2	Sequence 2, Appl
14	57	43.2	1005	2	US-08-469-537A-103	Sequence 103, App
15	56	42.4	24	6	5464756-1	Patent No. 5464756
16	55	41.7	877	2	US-08-673-789-2	Sequence 2, Appl
17	52	39.4	24	1	US-08-443-568B-4	Sequence 4, Appl
18	52	39.4	24	2	US-08-483-476-2	Sequence 2, Appl
19	52	39.4	24	2	US-08-484-219-2	Sequence 2, Appl
20	52	39.4	24	4	US-09-158-706-2	Sequence 2, Appl
21	52	39.4	24	5	PCT-US94-06997-4	Sequence 4, Appl
22	52	39.4	24	6	5464756-2	Patent No. 5464756
23	52	39.4	77	1	US-08-443-568B-10	Sequence 10, Appl
24	52	39.4	77	5	PCT-US94-06997-10	Sequence 10, Appl
25	52	39.4	150	1	US-08-443-568B-12	Sequence 12, Appl
26	52	39.4	150	5	PCT-US94-06997-12	Sequence 12, Appl
27	52	39.4	162	6	5464756-18	Patent No. 5464756

Query Match 47.7%; Score 63; DB 6; Length 24;
Best Local Similarity 52.6%; Pred. No. 0.029;
Matches 10; Conservative 4; Mismatches 5; Indels

RESULT 4
US-08-905-267-13
: Sequence 13, Application US/08905267
: Patent No. 5959075
: GENERAL INFORMATION:
: APPLICANT: Lok, Si
: APPLICANT: Conklin, Darrell C.
: APPLICANT: Adams, Robyn L.
: APPLICANT: Jelmberg, Anna C.

Query Match 44.7%; Score 59; DB 2; Length 188;
Best Local Similarity 45.0%; Pred. No. 0.7;

RESULT 8
5464756-4
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLIEN, RICHARD L.; WILKINS,
; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:

```

RESULT 11
US-08-442-248-2
; Sequence 2, Application US/08442248
; Patent No. 5759863
; GENERAL INFORMATION:
; APPLICANT: Caras, Ingrid W.
; APPLICANT: Winslow, John W.
; TITLE OF INVENTION: AL-1 Neurotrophic Factor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,248
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/330128
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: 920C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8674
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 928 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-442-248-2

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Query Match 43.2%; Score 57; DB 1; Length 928;
 Best Local Similarity 57.9%; Pred. No. 5.8;
 Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 6 LSSSCCKWGCSEISSLC 24
 |||||: ||: |||||
 Db 485 LSGSCCEGCGRA--SSLC 501

RESULT 12
 US-08-440-815-2
 ; Sequence 2, Application US/08440815
 ; Patent No. 5798448
 ; GENERAL INFORMATION:
 ; APPLICANT: Caras, Ingrid W.
 ; APPLICANT: Winslow, John W.
 ; TITLE OF INVENTION: AL-1 Neurotrophic Factor
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/440,815
 FILING DATE: 15-MAY-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/330128
 FILING DATE: 27-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Torchia, Timothy E.
 REGISTRATION NUMBER: 36,700
 REFERENCE/DOCKET NUMBER: 920C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/952-8674
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 928 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-440-815-2

Query Match 43.2%; Score 57; DB 1; Length 928;
 Best Local Similarity 57.9%; Pred. No. 5.8;
 Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 6 LSSSCCKWGCSEISSLC 24
 |||||: ||: |||||
 Db 485 LSGSCCEGCGRA--SSLC 501

RESULT 13
 US-08-486-449-2
 ; Sequence 2, Application US/08486449
 ; Patent No. 6280732
 ; GENERAL INFORMATION:
 ; APPLICANT: Caras, Ingrid W.
 ; APPLICANT: Winslow, John W.
 ; TITLE OF INVENTION: AL-1 Neurotrophic Factor
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/486,449
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/330128
 FILING DATE: 27-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Torchia, Timothy E.
 REGISTRATION NUMBER: 36,700
 REFERENCE/DOCKET NUMBER: P0920P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-8674
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 928 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-486-449-2

Query Match 43.2%; Score 57; DB 4; Length 928;
 Best Local Similarity 57.9%; Pred. No. 5.8;
 Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 6 LSSSCCKWGCSEISSLC 24
 |||||: ||: |||||
 Db 485 LSGSCCEGCGRA--SSLC 501

RESULT 14
 US-08-469-537A-103
 ; Sequence 103, Application US/08469537A
 ; Patent No. 5843749
 ; GENERAL INFORMATION:
 ; APPLICANT: Maisonnier, et al.
 ; TITLE OF INVENTION: EHK AND ROR TYROSINE
 ; TITLE OF INVENTION: KINASES
 ; NUMBER OF SEQUENCES: 107
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 ; STREET: 777 Old Saw Mill River Road
 ; CITY: Tarrytown
 ; STATE: NY
 ; COUNTRY: U.S.A.
 ; ZIP: 10591

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,537A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 08/406,247
 FILING DATE: 17-MAR-1995
 APPLICATION NUMBER: USSN 08/144,992
 FILING DATE: 28-OCT-1993
 APPLICATION NUMBER: USSN 07/736,559

;; FILING DATE: 26-JUL-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kempler, Ph.D., Gail M
;; REGISTRATION NUMBER: 32,143
;; REFERENCE/DOCKET NUMBER: REG 070C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 914-345-7400
;; TELEFAX: 914-345-7721
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 103:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1005 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-469-537A-103

Query Match 43.2%; Score 57; DB 2; Length 1005;
Best Local Similarity 57.9%; Pred. No. 6.3;
Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 6 LSSCCRWGCKSKSEISLC 24
|||: ||: |||
DB 596 LSGCCGCGGRA--SSLC 612

RESULT 15
5464756-1
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
; JAMES A.; VANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO: 1:
; LENGTH: 24
5464756-1

Query Match 42.4%; Score 56; DB 6; Length 24;
Best Local Similarity 42.1%; Pred. No. 0.24;
Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 6 LSSCCRWGCKSKSEISLC 24
||: ||: ||: ||: ||
DB 6 LSNKCHIGCTKKSLAKFC 24

Search completed: June 27, 2002, 16:08:44
Job time: 193 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2002, 16:09:27 ; Search time 36.01 Seconds
(without alignments)
64.042 Million cell updates/sec

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US-09-781-077-2_COPY_119_142
132
Title:
Perfect score:
Sequence: 1 DVLGLSSCCWGCCKSEISLC 24
Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

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Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	74	56.1	54	2	A26463	relaxin - spiny do	
2	66	50.0	48	2	A49739	relaxin - horse (f	
3	63	47.7	44	1	RXRKOT	relaxin - sand tig	
4	58	43.9	22	2	B58793	relaxin chain A -	
5	58	43.9	54	2	A32201	relaxin - Bryde's	
6	58	43.9	54	2	R32201	relaxin - minke wh	
7	58	43.9	182	1	RXP2	relaxin precursor	
8	57	43.2	59	2	A53879	relaxin - dog (fra	
9	57	43.2	186	1	RXRT	relaxin precursor	
10	57	43.2	893	2	S51603	receptor-like tyro	
11	57	43.2	898	2	S47489	receptor tyrosine	
12	57	43.2	1005	2	S49015	receptor tyrosine	
13	56	42.4	24	2	T32776	relaxin - baboon (
14	56	42.4	91	2	S73737	insulin homolog ce	
15	56	42.4	185	2	A34936	relaxin precursor	
16	55	41.7	877	2	I48967	brain-specific kin	
17	53	40.2	221	2	S07756	hypothetical prote	
18	52	39.4	24	2	S42780	relaxin - oranguta	
19	52	39.4	57	2	S42784	relaxin - gorilla	
20	52	39.4	145	2	S43224	insulin-related pr	
21	52	39.4	166	2	S42786	relaxin 2 precursor	
22	52	39.4	185	1	A60982	relaxin 2 precursor	
23	51	38.6	63	2	S00951	hypothetical prote	
24	51	38.6	1159	2	E83237	probable two-compo	
25	50	37.9	143	2	I47053	relaxin B,C and A	
26	50	37.9	399	2	T21586	hypothetical prote	
27	50	37.9	823	2	T34472	hypothetical prote	
28	49.5	37.5	448	2	T48214	endo-1,4-beta-mann	
29	49	37.1	64	2	A29543	relaxin - little s	

ALIGNMENTS

RESULT 1

A26643
relaxin - spiny dogfish (fragments)
C-Species: Squalus acanthias (spiny dogfish)
Date: 19-Nov-1988 #sequence_revision 26-May-1988
Accession: B26463; A26463
R: Bullesbach, E.E.; Gowan, L.K.; Schwabe, C.
Eur. J. Biochem. 161, 335-341, 1986
Title: Isolation, purification, and the
Reference number: A91179; MUID: 87054035
Accession: B26463

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Query Match          56.1%; Score 74; DB 2; Length 54;
Best Local Similarity 55.0%; Pred. No. 0.0024;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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QY	5	GLSS	SCCK	WGCS	CKSE	ISSLC	24
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Db	35	GMSS	KCC	TYG	CTRK	DISLC <td>54</td>	54

RESULT

A49739
relaxin - horse (fragments)
C:Species: Equus caballus (domestic horse)
C:Date: 07-Apr-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C:Cc:Accession: A49739
R:Stewart, D.R.; Nevins, B.; Hadas, E.; Vandlen, R.
R:Endocrinology 129, 375-383, 1991
A:Title: Affinity purification and sequence determination of equine relaxin.
A:Reference number: A49739; MUID:91275796
A:Accession: B49739
A:Molecule type: protein
A:Residues: 1-28 <STE>
A:Cc:Accession: A49739
A:Molecule type: protein

A;Cross-references: GB:K01088; NID:gl64634; PIDN:AAA31114.1; PID:gl64635
 R:James, R.; Niall, H.; Kwok, S.; Bryant-Greenwood, G.
 Nature 267, 544-546, 1977
 A;Title: Primary structure of porcine relaxin: homology with insulin and related growth
 A;Reference number: A93187; MUID:77213067
 A;Accession: A93187
 A;Molecule type: protein
 A;Residues: 25-50/'TWGR'/161-182 <JAM>
 R:Schwabe, C.; McDonald, J.K.; Steinmetz, B.G.
 Biochem. Biophys. Res. Commun. 75, 503-510, 1977
 A;Title: Primary structure of the B-chain of porcine relaxin.
 A;Reference number: A90205; MUID:77157271
 A;Accession: A90205
 A;Molecule type: protein
 A;Residues: 25-47/'VW'/50 <SCH1>
 R:Schwabe, C.; McDonald, J.K.
 Biochem. Biophys. Res. Commun. 74, 1501-1504, 1977
 A;Title: Demonstration of a pyroglutamyl residue at the N terminus of the B-chain of por
 A;Reference number: A90201; MUID:77134136
 A;Contents: annotation; pyrrolidone carboxylic acid
 R:Schwabe, C.; McDonald, J.K.; Steinmetz, B.G.
 Biochem. Biophys. Res. Commun. 70, 397-405, 1976
 A;Title: Primary structure of the A chain of porcine relaxin.
 A;Reference number: A90196; MUID:76231539
 A;Accession: A90196
 A;Molecule type: protein
 A;Residues: 161-169,'E',171-182 <SCH>
 R:Schwabe, C.; McDonald, J.K.
 Science 197, 914-915, 1977
 A;Title: Relaxin: a disulfide homolog of insulin.
 A;Reference number: A94245; MUID:77236040
 A;Contents: annotation; disulfide bonds
 R:Kohsaka, T.; Takahara, H.; Sugawara, K.; Tagami, S.
 Biol. Chem. Hoppe-Seyler 374, 203-210, 1993
 A;Title: Endogenous heterogeneity of relaxin and sequence of the major form in pregnant
 A;Reference number: S32312; MUID:93257096
 A;Accession: S32313
 A;Molecule type: protein
 A;Residues: 25-53 <KOH>
 A;Accession: S32312
 A;Molecule type: protein
 A;Residues: 161-182 <KO>
 R:Haley, J.; Crawford, R.; Hudson, P.; Scanlon, D.; Tregear, G.; Shine, J.; Niall, H.
 J. Biol. Chem. 262, 11940-11946, 1987
 A;Title: Porcine relaxin. Gene structure and expression.
 A;Reference number: A29796; MUID:87308187
 A;Accession: A29796
 A;Molecule type: DNA
 A;Residues: 1-115,'L',117-182 <HA2>
 A;Cross-references: GB:J02792; NID:gl64636; PIDN:AAA31115.1; PID:gl64637
 C;Comment: Relaxin is an ovarian hormone that acts with estrogen to produce dilation of
 C;Genetics: 70/1
 A;Introns: 70/1
 C;Superfamily: Insulin
 C;Keywords: pyroglutamic acid
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-56/Domain: relaxin chain B #status experimental <RCB>
 F;161-182/Domain: relaxin chain A #status experimental <MAT>
 F;161-182/Domain: relaxin chain A #status experimental <RCA>
 F;25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
 F;34-169,166-182,168-173/Disulfide bonds: #status experimental.

Query Match 43.9%; Score 58; DB 1; Length 182;
 Best Local Similarity 47.4%; Pred. No. 0.95;
 Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCSEISL 24
 || || : : : ||
 Db 164 LSEKCCQVGCIRKDIARLC 182

RESULT 8

A53879
 relaxin - dog (fragments)
 C;Species: Canis lupus familiaris (dog)
 C;Date: 27-Sep-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
 C;Accession: B53879; A53879
 J;Stewart, D.R.; Henzel, W.J.; Vandlen, R.
 J. Protein Chem. 11, 247-253, 1992
 A;Title: Purification and sequence determination of canine relaxin.
 A;Reference number: A53879; MUID:93000391
 A;Accession: B53879
 A;Molecule type: protein
 A;Residues: 1-35 <STE>
 A;Experimental source: placenta
 A;Note: sequence extracted from NCBI backbone (NCBIP:115401)
 A;Accession: A53879
 A;Molecule type: protein
 A;Residues: 36-59 <ST2>
 A;Experimental source: placenta
 A;Note: sequence extracted from NCBI backbone (NCBIP:115399)
 C;Superfamily: insulin
 C;Keywords: hormone
 F;1-35,36-59/Product: relaxin #status experimental <MAT>
 F;1-35/Domain: chain B #status experimental <CHB>
 F;36-59/Domain: chain A #status experimental <CHA>
 F;9-46,21-59,45-50/Disulfide bonds: #status predicted

Query Match 43.2%; Score 57; DB 2; Length 59;
 Best Local Similarity 42.1%; Pred. No. 0.53;
 Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCSEISL 24
 : || || : : : ||
 Db 41 MSDKCCNVGCTRELASRC 59

RESULT 9
RXRT

relaxin precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 24-Sep-1999
 C;Accession: A01614
 R:Hudson, P.; Haley, J.; Cronk, M.; Shine, J.; Niall, H.
 Nature 291, 127-131, 1981
 A;Title: Molecular cloning and characterization of cDNA sequences coding for rat rela
 A;Reference number: A01614; MUID:81197624
 A;Accession: A01614
 A;Molecule type: mRNA
 A;Residues: 1-186 <HUD>
 A;Cross-references: GB:J00780; GB:M25468; NID:g206606; PIDN:AAA42029.1; PID:g206607
 C;Superfamily: insulin
 C;Keywords: hormone; ovary; pyroglutamic acid

F;1-22/Domain: signal sequence #status predicted <SIG>
 F;23-57/Domain: relaxin chain B #status predicted <RXB>
 F;58-162/Domain: relaxin #status predicted <MAT>
 F;163-186/Domain: relaxin connecting C peptide #status predicted <RXC>
 F;36-173,48-186,172-177/Disulfide bonds: #status predicted
 F;163/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predi

Query Match 43.2%; Score 57; DB 1; Length 186;
 Best Local Similarity 47.4%; Pred. No. 1.3;
 Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCSEISL 24
 || || || : : : ||
 Db 168 LSEQCHIGCTRRSTAKLC 186

RESULT 10

S51603
 receptor-like tyrosine kinase Etk-1 - rat

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
 C:Accession: S51603
 R:Maisonnier, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.
 Oncogene 8, 3277-3288, 1993
 A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase family
 A:Reference number: S49015; MUID:94067777
 A:Accession: S51603
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-893 <MAI>
 A:Cross-references: EMBL:S68028
 A:Note: the authors translated the codon GAC for residue 170 as Glu
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C:Keywords: ATP; transmembrane protein
 F:563-829/Domain: protein kinase homology <KIN>
 F:571-579/Region: protein kinase ATP-binding motif

Query Match 43.2%; Score 57; DB 2; Length 893;
 Best Local Similarity 57.9%; Pred. No. 4.6;
 Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 6 LSSSCCKWGCCKSKSEISSLC 24
 |||||: ||: |||||
 Db 484 LSGSCCEGCGRA--SSLC 500

RESULT 11

S47489
 receptor tyrosine kinase - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
 C:Accession: S47489
 R:Taylor, V.; Pfaff, S.; Miescher, G.C.; Honegger, P.; Breitschopf, H.; Lassmann, H.; St
 submitted to the EMBL Data Library, April 1994
 A:Description: Expression and developmental regulation of EHK-1, a neuronal ELK-like rec
 A:Reference number: S47489
 A:Accession: S47489
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-898 <TA>
 A:Cross-references: EMBL:X78689; NID:g531543; PIDN:CAA55357.1; PID:g531544
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C:Keywords: ATP; transmembrane protein
 F:568-834/Domain: protein kinase homology <KIN>
 F:576-584/Region: protein kinase ATP-binding motif

Query Match 43.2%; Score 57; DB 2; Length 898;
 Best Local Similarity 57.9%; Pred. No. 4.6;
 Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 6 LSSSCCKWGCCKSKSEISSLC 24
 |||||: ||: |||||
 Db 489 LSGSCCEGCGRA--SSLC 505

RESULT 12

S49015
 receptor tyrosine kinase Etk-1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
 C:Accession: S49015; S51602
 R:Maisonnier, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.
 Oncogene 8, 3277-3288, 1993
 A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam
 A:Reference number: S49015; MUID:94067777
 A:Accession: S49015
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1005 <MAI>
 A:Cross-references: EMBL:S68024

A:Note: the authors translated the codon GAC for residue 170 as Glu
 A:Accession: S51602
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-305, 'G', 359-1005 <MA2>
 A:Cross-references: EMBL:S68026
 A:Note: the authors translated the codon GAC for residue 170 as Glu
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
 C:Keywords: ATP; transmembrane protein
 F:675-941/Domain: protein kinase homology <KIN>
 F:683-691/Region: protein kinase ATP-binding motif

Query Match 43.2%; Score 57; DB 2; Length 1005;
 Best Local Similarity 57.9%; Pred. No. 5;
 Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 6 LSSSCCKWGCCKSKSEISSLC 24
 |||||: ||: |||||
 Db 596 LSGSCCEGCGRA--SSLC 612

RESULT 13

S42776
 relaxin - baboon (fragment)
 C:Species: Papio sp. (baboon)
 C:Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
 C:Accession: S42776
 R:Evans, B.B.
 submitted to the EMBL Data Library, November 1993
 A:Reference number: S42776
 A:Accession: S42776
 A:Molecule type: DNA
 A:Residues: 1-24 <EVA>
 A:Cross-references: EMBL:Z27106; NID:g415396; PIDN:CAA81622.1; PID:g415397
 C:Genetics:
 C:Superfamily: insulin
 C:Keywords: disulfide bond; hormone
 F:1-24/Domain: relaxin chain A (fragment) #status predicted <RXA>

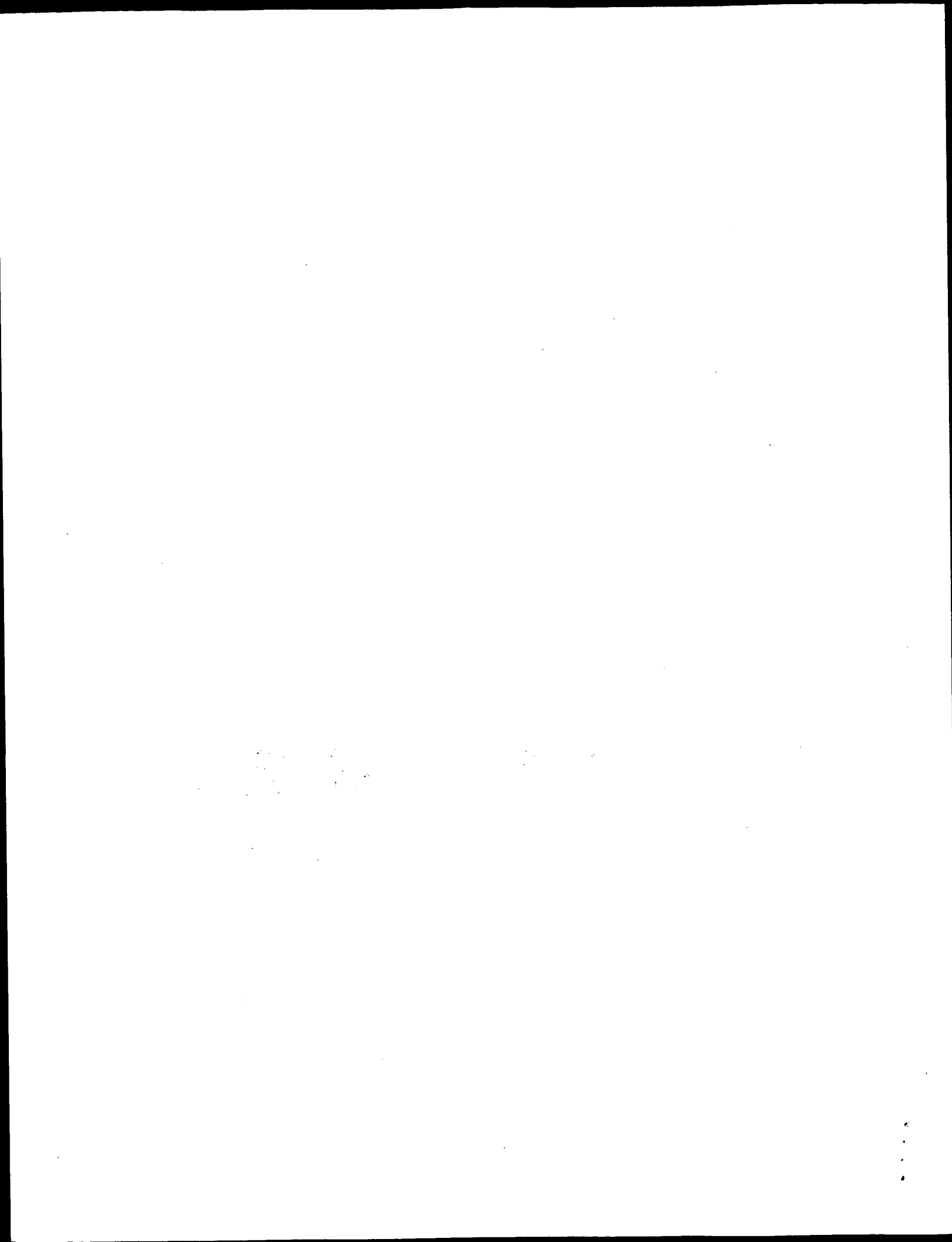
Query Match 42.4%; Score 56; DB 2; Length 24;
 Best Local Similarity 42.1%; Pred. No. 0.36;
 Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCCKSKSEISSLC 24
 ||: || ||: ||: ||
 Db 6 LSNKCHIGCTKKLAKFC 24

RESULT 14

T37327
 insulin homolog ceinsulin-3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-Jan-2000
 C:Accession: T37327; T15535
 R:Kawano, T.
 submitted to the EMBL Data Library, September 1999
 A:Description: MRNA for a putative insulin-like peptide of Caenorhabditis elegans.
 A:Reference number: Z21691
 A:Accession: T37327
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-91 <KAW>
 A:Cross-references: EMBL:AB032258; PIDN:BAA84470.1
 R:Du, Z.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid C17C3.
 A:Reference number: Z18366
 A:Accession: T15535
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA

Search completed: June 27, 2002, 16:09:28
Job time: 212 sec



ID AC RELX_HORSE STANDARD; PRT; 182 AA.
P22969; Q28907;
01-AUG-1991 (Rel. 19, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Prorelaxin precursor (RXN).
GN RLN.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HOKKAIDO; TISSUE=Placenta;
RA Min K., Shiota K., Ogawa T.;
RT "Molecular cloning of equine preprorelaxin cDNA.";
RL J. Reprod. Dev. 42:171-178(1996).
RN [2]
RP SEQUENCE OF 32-174 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95359320; PubMed=7543295;
RA Klonisch T., Ryan P.L., Yamashiro S., Porter D.G.;
RT "Partial complementary deoxyribonucleic acid cloning of equine relaxin
messenger ribonucleic acid, and its localization within the equine
placenta.";
RL Biol. Reprod. 52:1307-1315(1995).
RN [3]
RP SEQUENCE OF 26-53 AND 163-182.
RC TISSUE=Placenta;
RX MEDLINE=91275796; PubMed=2055195;
RA Stewart D.R., Nevins B., Hadas E., Vandlen R.;
RT "Affinity purification and sequence determination of equine relaxin.";
RL Endocrinology 129:375-383(1991).
CC -!- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN
TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.
CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
DISULFIDE BONDS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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CC
CC EMBL; AB000201; BAA19069.1; -
DR EMBL; S78800; AAB35036.1; -
DR PIR; A49739; A49739.
DR PIR; B49739; B49739.
DR HSP; P01348; 4RLX.
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR Pfam; PF00049; Insulin; 1.
DR SMART; SM00078; ILGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Signal.
FT SIGNAL 1 25
FT CHAIN 26 53 RELAXIN B CHAIN.
FT PROPEP 54 156 CONNECTING PEPTIDE.
FT CHAIN 161 182 RELAXIN A CHAIN.
FT DISULFID 35 169 INTERCHAIN (BY SIMILARITY).
FT DISULFID 47 182 INTERCHAIN (BY SIMILARITY).
FT DISULFID 168 173 BY SIMILARITY.
FT CONFLICT 66 66 A -> V (IN REF. 2).
FT CONFLICT 133 133 L -> Q (IN REF. 2).
SQ SEQUENCE 182 AA; 20721 MW; E5C941430A838B6 CRC64;

Query Match 50.0%; Score 66; DB 1; Length 182;
Best Local Similarity 47.4%; Pred. No. 0.011;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 LSSCKCKWGCKSKSEISL 24
Db 164 LSHCCYWGCTKRRLARQC 182

RESULT 3
RELX_ODOTA STANDARD; PRT; 44 AA.
ID RELX_ODOTA
AC P01349;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Relaxin (Fragments).
OS Odontaspis taurus (Sand tiger shark) (Eugomphodus taurus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes; Odontaspidae;
OC Carcharias.
OX NCBI_TaxID=30501;
RN [1]
RP SEQUENCE.
RX MEDLINE=82004703; PubMed=7274472;
RA Gowan L.K., Reining J.W., Schwabe C., Bedarkar S., Blundell T.L.;
RT "On the primary and tertiary structure of relaxin from the sand tiger
shark (Odontaspis taurus).";
RL Eur. J. Biochem. 161:335-341(1986).
CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
DISULFIDE BONDS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC PIR; A01616; RARKOT.
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR Pfam; PF00049; Insulin; 1.
DR SMART; SM00078; ILGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone.
FT NON_CONS 1 20 RELAXIN B CHAIN.
FT CHAIN 20 21
FT NON_CONS 21 44
FT CHAIN 21 44 RELAXIN A CHAIN.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 3 31 INTERCHAIN (BY SIMILARITY).
FT DISULFID 15 44 INTERCHAIN (BY SIMILARITY).
FT DISULFID 30 35 BY SIMILARITY.
SQ SEQUENCE 44 AA; 4730 MW; 6122F6604C660607 CRC64;

Query Match 47.7%; Score 63; DB 1; Length 44;
Best Local Similarity 52.6%; Pred. No. 0.0089; 5; Indels 0; Gaps 0;
Matches 10; Conservative 4; Mismatches 5;

QY 6 LSSCKCKWGCKSKSEISL 24
Db 26 MSIKCCYWGCTKRKDISVL 44

RESULT 4
INL5_MOUSE STANDARD; PRT; 135 AA.
ID INL5_MOUSE
AC Q9WUG6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Insulin-like peptide INSL5 precursor (insulin-like peptide 5)
(Relaxin/insulin-like protein) (Relaxin/insulin-like factor 2).
DE


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QY 5 GLSSCKWGCSEISL 24
   ||| ||| ||| ||| |||
Db 173 GYSEKCLTGTCTKEELSIAC 192

RESULT 6
C59B_MOUSE
ID C59B_MOUSE STANDARD; PRT; 129 AA.
AC P58019;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C59B glycoprotein precursor (Membrane attack complex inhibition
DE factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
GN C59B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=20403635; PubMed=10946279;
RA Qian Y.-M., Qin X., Miwa T., Sun X., Halperin J.A., Song W.-C.;
RT "Identification and functional characterization of a new gene encoding
RT the mouse terminal complement inhibitor CD59.";
RL J. Immunol. 165:2528-2534(2000).
CC -!- FUNCTION: POTENT INHIBITOR OF THE COMPLEMENT MEMBRANE ATTACK
CC COMPLEX (MAC) ACTION. ACTS BY BINDING TO THE C8 AND/OR C9
CC COMPLEMENTS OF THE ASSEMBLING MAC, THEREBY PREVENTING
CC INCORPORATION OF THE MULTIPLE COPIES OF C9 REQUIRED FOR COMPLETE
CC FORMATION OF THE OSMOTIC PORE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- TISSUE SPECIFICITY: SPECIFICALLY IN TESTIS.
CC -!- SIMILARITY: CONTAINS 1 UPAR/LY6 DOMAIN.
DR MGD; MGI:1888996; CD59b.
DR InterPro: IPR001526; LY6-UPAR.
DR Pfam: PF00021; UPAR_LY6; 1.
DR ProDom: PD003128; LY6_CD59; 1.
DR SMART; SM00134; LY6; 1.
DR PROSITE; PS00983; LY6-UPAR; FALSE_NEG.
KW Antigen; Glycoprotein; GPI-anchor; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 107 CD59B GLYCOPROTEIN.
FT PROPEP 108 129 REMOVED IN MATURE FORM (BY SIMILARITY).
FT DOMAIN 24 107 UPAR/LY6.
FT DISULFID 26 49 BY SIMILARITY.
FT DISULFID 29 36 BY SIMILARITY.
FT DISULFID 42 62 BY SIMILARITY.
FT DISULFID 68 86 BY SIMILARITY.
FT DISULFID 87 92 BY SIMILARITY.
FT CARBOHYD 39 39 N-LINKED (GLCNAC... ) (POTENTIAL).
FT LIPID 107 107 GPI-ANCHOR (BY SIMILARITY).
SQ SEQUENCE 129 AA; 14266 MW; 2D619096A9C9CEE CRC64;

Query Match 45.1%; Score 59.5; DB 1; Length 129;
Best Local Similarity 40.6%; Pred. No. 0.071;
Matches 13; Conservative 5; Mismatches 3; Indels 11; Gaps 2;

QY 3 LAGLSCKWGCSEISL 23
   ||| ||| ||| ||| |||
Db 79 VAGIQSKCCWGLCNKLDGLPEPNAETSSL 110

RESULT 7
INL6_RAT
ID INL6_RAT STANDARD; PRT; 188 AA.
AC Q9W41;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

Insulin-like peptide INSL6 precursor (Insulin-like peptide 6).
INSL6.
Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RX MEDLINE=20297000; PubMed=10819760;
RA Lok S., Johnston D.S., Conklin D., Lofton-Day C.E., Adams R.L.,
RA Jelmberg A.C., Whitmore T.E., Schrader S., Griswold M.D.,
RA Jaspers S.R.;
RT "Identification of INSL6, a new member of the insulin family that is
RT expressed in the testis of the human and Rat.";
RL Biol. Reprod. 62:1593-1599(2000).
CC -!- FUNCTION: MAY HAVE A ROLE IN SPERM DEVELOPMENT AND FERTILIZATION.
CC -!- SUBCELLULAR LOCATION: TESTIS- AND PROSTATE-SPECIFIC.
CC -!- TISSUE SPECIFICITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC
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CC
CC EMBL: AF159506; AAD40956.1;
CC InterPro: IPR000739; Insulin_IGF_relaxin.
CC Pfam: PF00049; Insulin; 1.
CC SMART; SM00078; ILGF; 1.
CC PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Signal; Cleavage on pair of basic residues.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 188 INSULIN-LIKE PEPTIDE INSL6.
FT CHAIN 23 51 INSULIN-LIKE PROTEIN INSL6 B CHAIN
(POTENTIAL).
FT PROPEP 53 158 INSULIN-LIKE PROTEIN INSL6 C CHAIN
(POTENTIAL).
FT CHAIN 163 188 INSULIN-LIKE PROTEIN INSL6 A CHAIN
(POTENTIAL).
FT MOD_RES 23 23 PYRROLIDONE CARBOXYLIC ACID (BY
SIMILARITY).
FT DISULFID 33 169 BY SIMILARITY.
FT DISULFID 45 182 BY SIMILARITY.
FT DISULFID 168 173 BY SIMILARITY.
SQ SEQUENCE 188 AA; 21442 MW; 50212AB3CE9982B3 CRC64;

Query Match 44.7%; Score 59; DB 1; Length 188;
Best Local Similarity 45.0%; Pred. No. 0.12;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 5 GLSSCKWGCSEISL 24
   ||| ||| ||| ||| |||
Db 163 GFADKCAIGCSREELAVAC 182

RESULT 8
RELX_BALAC
ID RELX_BALAC STANDARD; PRT; 54 AA.
AC P1184;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Relaxin.
OS Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaenopteridae; Balaenoptera.
OX NCBI_TaxID=9767;

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RN SEQUENCE.
RX MEDLINE=89093167; PubMed=2910872;
RA Schwabe C., Bullesbach E.E., Heyn H., Yoshioka M.;
RT "Cetacean relaxin. Isolation and sequence of relaxins from
RT Balaenoptera acutorostrata and Balaenoptera edeni.";
RL J. Biol. Chem. 264:940-943(1989).
CC -1- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN
CC TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.
CC -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR PIR: B32201; B32201.
DR HSP: P01348; 4RLX.
DR InterPro: IPR000739; Insulin_IGF_relaxin.
DR Pfam: PF00049; Insulin; 1.
DR SMART: SM00078; ILGF; 1.
DR PROSITE: PS00262; INSULIN; 1.
KW Insulin family; Hormone.
FT CHAIN 1 32 RELAXIN B CHAIN.
FT NON_CONS 32 33
FT CHAIN 33 54 RELAXIN A CHAIN.
FT DISULFID 10 41 INTERCHAIN.
FT DISULFID 22 54 INTERCHAIN.
FT DISULFID 40 45
SQ SEQUENCE 54 AA; 6099 MW; DC2672CB940F59BE CRC64;

Query Match 43.9%; Score 58; DB 1; Length 54;
Best Local Similarity 47.4%; Pred. No. 0.055;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 LSSSCCKWCKSKSEISSLC 24
|| ||: ||: ||: ||
Db 36 LSEKCCQVGCIRKDIARLC 54

RESULT 9
RELX_BALED STANDARD; PRT; 54 AA.
AC P11185;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Relaxin.
OS Balaenoptera edeni (Bryde's whale).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaenopteridae; Balaenoptera.
OX NCBI_TaxID=9769;
RN [1]
RP SEQUENCE.
RX MEDLINE=89093167; PubMed=2910872;
RA Schwabe C., Bullesbach E.E., Heyn H., Yoshioka M.;
RT "Cetacean relaxin. Isolation and sequence of relaxins from
RT Balaenoptera acutorostrata and Balaenoptera edeni.";
RL J. Biol. Chem. 264:940-943(1989).
CC -1- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN
CC TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.
CC -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR PIR: A32201; A32201.
DR HSP: P01348; 4RLX.
DR InterPro: IPR000739; Insulin_IGF_relaxin.
DR Pfam: PF00049; Insulin; 1.
DR SMART: SM00078; ILGF; 1.
DR PROSITE: PS00262; INSULIN; 1.
KW Insulin family; Hormone.
FT CHAIN 1 32 RELAXIN B CHAIN.
FT NON_CONS 32 33

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FT CHAIN 33 54 RELAXIN A CHAIN.
FT DISULFID 10 41 INTERCHAIN.
FT DISULFID 22 54 INTERCHAIN.
FT DISULFID 40 45
SQ SEQUENCE 54 AA; 6072 MW; DB5535F8951F49BE CRC64;

Query Match 43.9%; Score 58; DB 1; Length 54;
Best Local Similarity 47.4%; Pred. No. 0.055;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 LSSSCCKWCKSKSEISSLC 24
|| ||: ||: ||: ||
Db 36 LSEKCCQVGCIRKDIARLC 54

RESULT 10
RELX_PIG STANDARD; PRT; 182 AA.
AC P01348;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pror relaxin precursor.
DE RLN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87308187; PubMed=2442155;
RA Haley J., Crawford R., Hudson P., Scanlon D., Tregear G., Shine J.,
RA Niall H.;
RT "Porcine relaxin. Gene structure and expression.";
RL J. Biol. Chem. 262:11940-11946(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157118; PubMed=6897721;
RA Haley J., Hudson P., Scanlon D., John M., Cronk M., Shine J.,
RA Tregear G., Niall H.;
RT "Porcine relaxin: molecular cloning and cDNA structure.";
RL DNA 1:155-162(1982).
RN [3]
RP PRELIMINARY SEQUENCE OF 25-54 AND 161-182.
RX MEDLINE=77213067; PubMed=876374;
RA James R., Niall H., Kwok S., Bryant-Greenwood G.;
RT "Primary structure of porcine relaxin: homology with insulin and
RT related growth factors.";
RL Nature 267:544-546(1977).
RN [4]
RP SEQUENCE OF 25-51.
RX MEDLINE=7157271; PubMed=851452;
RA Schwabe C., McDonald J.K., Steinetz B.G.;
RT "Primary structure of the B-chain of porcine relaxin.";
RL Biochem. Biophys. Res. Commun. 75:503-510(1977).
RN [5]
RP SEQUENCE OF 25.
RX MEDLINE=77134136; PubMed=843375;
RA Schwabe C., McDonald J.K.;
RT "Demonstration of a pyroglutamyl residue at the N terminus of the B-
RT chain of porcine relaxin.";
RL Biochem. Biophys. Res. Commun. 74:1501-1504(1977).
RN [6]
RP SEQUENCE OF 161-182.
RX MEDLINE=76231539; PubMed=938497;
RA Schwabe C., McDonald J.K., Steinetz B.G.;
RT "Primary structure of the A chain of porcine relaxin.";
RL Biochem. Biophys. Res. Commun. 70:397-405(1976).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=77236040; PubMed=887933;
RA Schwabe C., McDonald J.K.;

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RT "Relaxin: a disulfide homolog of insulin."; Science 197:914-915(1977).
RL [8]
RN 3D-STRUCTURE MODELING.
RP MEDLINE=78092399; PubMed=622170;
RX Isaacs N.W., James R., Niall H., Bryant-Greenwood G., Dodson G.G.,
RA Evans A., North A.C.T.;
RA "Relaxin and its structural relationship to insulin.";
RT Nature 271:278-281(1978).
RL Nature 271:278-281(1978).
CC -1- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN
CC TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.
CC -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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CC EMBL; K01088; AAA31114.1; -
CC EMBL; J02792; AAA31115.1; -
CC EMBL; A16593; CAA01295.1; -
CC EMBL; A06852; CAA00600.1; -
CC PIR; A01615; RXPG.
CC PIR; A29796; A29796.
CC PDB; 1RLX; 15-OCT-94.
CC PDB; 2RLX; 15-OCT-94.
CC PDB; 3RLX; 15-OCT-94.
CC PDB; 4RLX; 15-OCT-94.
CC InterPro; IPR000739; Insulin_IGF_relaxin.
CC Pfam; PF00049; Insulin; 1.
CC SMART; SM00078; ILGF; 1.
CC PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Signal; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 56 RELAXIN B CHAIN.
FT PROPEP 57 154 CONNECTING PEPTIDE.
FT CHAIN 161 182 RELAXIN A CHAIN.
FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 34 169 INTERCHAIN.
FT DISULFID 46 182 INTERCHAIN.
FT DISULFID 168 173
FT CONFLICT 47 47 G -> GVWS (IN REF. 4).
FT CONFLICT 51 54 WGR -> TWGR (IN REF. 3).
FT CONFLICT 116 116 S -> L (IN REF. 1).
FT CONFLICT 170 170 Q -> E (IN REF. 6).
SQ SEQUENCE 182 AA; 20818 MW; 20736EB089F13AB4 CRC64;

Query Match 43.98; Score 58; DB 1; Length 182;
Best Local Similarity 47.4%; Pred. No. 0.16;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCCKSKSEISL 24
DB 164 LSEKCCQVGCIRKDIARLC 182

RESULT 11
INL5_HUMAN
ID INL5_HUMAN STANDARD; PRT; 135 AA.
AC Q9Y506;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Insulin-like peptide INSL5 precursor (Insulin-like peptide 5).
GN INSL5.
OS Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
TISSUE-Colon;
MEDLINE=99389725; PubMed=10458910;
RA Conklin D., Lofton-Day C.E., Haldeman B.A., Ching A., Whitmore T.E.,
RA Lok S., Jaspers S.;
RA "Identification of INSL5, a new member of the insulin superfamily.";
Genomics 60:50-56(1999).
RL -1- FUNCTION: MAY HAVE A ROLE IN GUT CONTRACTILITY OR IN THYMIC
CC DEVELOPMENT AND REGULATION.
CC -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN RECTUM WITH LOWER LEVELS
CC IN UTERUS AND ASCENDING AND DESCENDING COLON.
CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC
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CC
CC EMBL; AF133816; AAD29686.1; -
CC MIM; 606413; -
CC InterPro; IPR000739; Insulin_IGF_relaxin.
CC SMART; SM00078; ILGF; 1.
CC PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Signal.
FT SIGNAL 1 18
FT CHAIN 19 48 INSULIN-LIKE PEPTIDE INSL5 B CHAIN
FT PROPEP 49 114 CONNECTING PEPTIDE (POTENTIAL).
FT CHAIN 115 135 INSULIN-LIKE PEPTIDE INSL5 A CHAIN
FT DISULFID 29 122 INTERCHAIN (BY SIMILARITY).
FT DISULFID 41 135 INTERCHAIN (BY SIMILARITY).
FT DISULFID 121 126 BY SIMILARITY.
SQ SEQUENCE 135 AA; 15318 MW; 98FFCB20E9C4BC1F CRC64;

Query Match 43.2%; Score 57; DB 1; Length 135;
Best Local Similarity 47.4%; Pred. No. 0.17;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCCKSKSEISL 24
DB 117 LQFLCCTGCGSMTDLALC 135

RESULT 12
RELX_CANFA
ID RELX_CANFA STANDARD; PRT; 177 AA.
AC Q9TRM8; Q9TRM9; Q9N0Z7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Prorelaxin precursor.
GN RLN.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Placenta;
RX MEDLINE=99150177; PubMed=10026098;
RA Klonisch T., Hombach-Klonisch S., Froehlich C., Kauffold J.,
RA Steger K., Steinetz B.G., Fischer B.;

1000

100

[2] SEQUENCE FROM N.A. (ISOFORM 6).
STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
MEDLINE=95206467; PubMed=7898646;
Taylor V., Miescher G.C., Pfarr S., Honegger P., Breitschopf H.,
Lassmann H., Steck A.J.;
"Expression and developmental regulation of Etk-1, a neuronal
Etk-like receptor tyrosine kinase in brain."
Neuroscience 63:163-178(1994).
-1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
EPHRIN-A1, -A2, -A3, -A4 AND -A5.
-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- ALTERNATIVE PRODUCTS: 6 ISOFORMS; 1 (SHOWN HERE), 2, 3, 4, 5 AND
6; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS
SYSTEM. PROMINANTLY EXPRESSED IN NEURONS.
-1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
RECEPTOR SUBFAMILY.

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EMBL; X78689; CAA55357.1; -
HSP; P29323; 18AF
InterPro; IPR000561; EGF-like.
InterPro; IPR001090; Ephrin-receptor.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR003961; FN_III.
InterPro; IPR003962; FNIII_repeat.
InterPro; IPR001426; Receptor_tyr_kin_v.
InterPro; IPR001660; SAM.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF01404; EPH_1bd; 1.
Pfam; PF00041; fn3; 2.
Pfam; PF00069; pkinase; 1.
Pfam; PF00536; SAM; 1.
PRINTS; PR00014; FNTYPEIII.
PRINTS; PR00109; TYRKINASE.
ProDom; PD001495; Ephrin_rcptor; 1.
SMART; SM00001; EGF_like; 1.
SMART; SM00060; FN3; 2.
SMART; SM00219; Tyrc; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS0105; SAM_DOMAIN; 1.
Transferase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
Alternative splicing.
SIGNAL 1 26
CHAIN 27 1005
FT CHAIN 27 1005 EPHRIN TYPE-A RECEPTOR 5.
FT DOMAIN 27 575 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 576 596 POTENTIAL.
FT DOMAIN 597 1005 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 222 356 CYS-RICH.
FT DOMAIN 357 466 FIBRONECTIN TYPE-III 1.
FT DOMAIN 467 563 FIBRONECTIN TYPE-III 2.
FT DOMAIN 677 938 PROTEIN KINASE.
FT DOMAIN 967 1005 SAM.
FT NP_BIND 683 691 ATP (BY SIMILARITY).
FT BINDING 709 709 ATP (BY SIMILARITY).
FT

ACT_SITE 802
MOD_RES 652
MOD_RES 658
MOD_RES 835
MOD_RES 835
MOD_RES 984
CARBOHYD 266
CARBOHYD 301
CARBOHYD 371
CARBOHYD 425
CARBOHYD 438
CARBOHYD 463
VARSPPLIC 10
VARSPPLIC 306
VARSPPLIC 357
VARSPPLIC 358
VARSPPLIC 597
CONFLICT 170
CONFLICT 566
CONFLICT 578
CONFLICT 669
CONFLICT 708
CONFLICT 979
SEQUENCE 1005 AA; 111007 MW; 1AED42C99693C574 CRC64;
Query Match 43.2%; Score 57; DB 1; Length 1005;
Best Local Similarity 57.9%; Pred. No. 0.94;
Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
QY 6 LSSSCCKWCKSKSEISLILC 24
Db 596 LSGSCCECGCGRA--SSLC 612
RESULT 15
ID EPA5_HUMAN STANDARD; PRT; 1037 AA.
AC P54756;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ephrin type-A receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein-
DE kinase receptor EHK-1) (Eph homology kinase-1) (Receptor protein-
DE tyrosine kinase HEK7).
GN EPHA5 OR EHK1 OR HEK7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Miescher G.C.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RP SEQUENCE OF 25-1037 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95206782; PubMed=7898931;
RA Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
RA Basu R., Weicher A.A.;
RT "cDNA cloning and tissue distribution of five human EPH-like receptor
RT protein-tyrosine kinases."
RL Oncogene 10:897-905(1995).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC

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OM protein - protein search, using sw model

Run on: June 27, 2002, 16:16:29 ; Search time 58.57 Seconds
(without alignments)
70.887 Million cell updates/sec

Title: US-09-781-077-2_COPY_119_142

Perfect score: 132

Sequence: 1 DVLGLSSCKWCKSKSEISL 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	47.7	155	13 Q9DEP8	Q9dep8 rana esculenta
2	58	43.9	22	6 Q9TRG6	Q9trg6 sus scrofa
3	57	43.2	180	6 Q9MYK8	Q9myk8 felis silve
4	56	42.4	24	6 Q28787	Q28787 papio hamad
5	56	42.4	199	6 Q9NOT9	Q9not9 camelus dro
6	52.5	39.8	129	11 Q920G7	Q920g7 mus musculu
7	52	39.4	24	6 Q28430	Q28430 gorilla gor
8	52	39.4	24	6 Q28781	Q28781 pongo pygma
9	51.5	39.0	868	5 Q9WIA5	Q9wia5 drosophila
10	51	38.6	262	10 Q9LV78	Q9lv78 arabidopsis
11	51	38.6	370	5 Q95VP6	Q95vp6 leishmania
12	51	38.6	1159	16 Q9HYX0	Q9hyx0 pseudomonas
13	50	37.9	399	5 Q62189	Q62189 caenorhabdi
14	50	37.9	823	5 Q23141	Q23141 caenorhabdi
15	49.5	37.5	448	10 Q9LZV3	Q9lzv3 arabidopsis
16	49	37.1	169	4 Q14564	Q14564 homo sapien

17	49	37.1	272	11 Q99L19	Q99l19 mus musculu
18	49	37.1	362	11 Q35281	Q35281 mus musculu
19	49	37.1	2872	11 Q9WUH8	Q9wh8 rattus norv
20	49	37.1	3857	11 Q88840	Q88840 mus musculu
21	48	36.4	56	5 Q95S27	Q95s27 drosophila
22	48	36.4	127	13 Q90WX8	Q90wx8 xenopus lae
23	48	36.4	188	6 Q9GK46	Q9gk46 galago cras
24	48	36.4	332	10 Q65485	Q65485 arabidopsis
25	48	36.4	444	12 Q9YTK1	Q9ytk1 ateline her
26	48	36.4	459	4 Q92577	Q92577 homo sapien
27	48	36.4	686	4 Q15061	Q15061 homo sapien
28	48	36.4	2233	5 Q94711	Q94711 paramecium
29	47.5	36.0	205	5 Q9BK18	Q9bk18 acropora mi
30	47.5	36.0	735	11 Q9D4G3	Q9d4g3 mus musculu
31	47.5	36.0	735	11 Q9QWJ0	Q9qw10 mus musculu
32	47.5	36.0	735	11 Q60718	Q60718 mus musculu
33	47.5	36.0	2809	4 Q96JP8	Q96jp8 homo sapien
34	47	35.6	108	5 Q20896	Q20896 caenorhabdi
35	47	35.6	118	10 Q9S979	Q9s979 crambe abys
36	47	35.6	131	6 Q9N0Z8	Q9n0z8 capra hircu
37	47	35.6	131	6 Q9N0T8	Q9n0t8 dama dama
38	47	35.6	131	6 Q9GK47	Q9gk47 galago cras
39	47	35.6	179	5 Q23203	Q23203 caenorhabdi
40	47	35.6	195	5 Q16759	Q16759 caenorhabdi
41	47	35.6	251	5 Q9T225	Q9t225 caenorhabdi
42	47	35.6	464	10 Q41064	Q41064 pisum sativ
43	47	35.6	718	3 Q96VZ6	Q96vz6 cryptococcu
44	47	35.6	2621	10 Q9LM23	Q9lmz3 arabidopsis
45	47	35.6	2658	10 Q9SGE4	Q9sge4 arabidopsis

ALIGNMENTS

RESULT 1
Q9DEP8 PRELIMINARY; PRT; 155 AA.
ID Q9DEP8
AC Q9DEP8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RELAXIN-LIKE PROTEIN.
GN INSL3.
OS Rana esculenta (Edible frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8401;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=21309007; PubMed=11416046;
RA De Rienzo G., Aniello F., Branno M., Minucci S.;
RT "Isolation and characterization of a novel member of the relaxin/insulin family from the testis of the frog Rana esculenta.";
RL Endocrinology 142:3231-3238(2001).
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR EMBL: AJ298874; CAC16108.1;
DR InterPro: IPR000739; Insulin_IGF-relaxin.
DR InterPro: IPR002052; N6_Mtase.
DR Pfam: PF00049; Insulin; 1.
DR SMART: SM00078; IIGF; 1.
DR PROSITE: PS00092; N6_MTASE; UNKNOWN_1.
SQ SEQUENCE 155 AA; 17470 MW; 517ADA5385026E34 CRC64;

Query Match Best Local Similarity 47.7%; Score 63; DB 13; Length 155;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 4 AGLSSSCCKWCKSKSEISL 24
DB 135 AGPALSCCQRCGRKRLMKFC 155

Best Local Similarity 44.4%; Pred. NO. 0.21;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 7 SSSCCWGCSEISSLC 24
DB 163 SDRCCNVGCTRELADLC 180

RESULT 4

ID Q28787 PRELIMINARY; PRT; 24 AA.
AC Q28787;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RELAXIN (FRAGMENT).
GN RLX.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BABA;
RA Evans B.B.A., Fu P., Tregear G.G.W.;
RT "Characterisation of primate relaxin genes."
RL J. Mol. Endocrinol. 0:0-0(1993).
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR EMBL; Z27106; CAAB1622.1; -.
DR HSP; P04090; 6RLX.
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR PROSITE; PS00262; INSULIN; 1.
FT NON_TER 1
SQ SEQUENCE 24 AA; 2691 MW; 560BC26A8BADBA14 CRC64;

Query Match 42.4%; Score 56; DB 6; Length 24;
Best Local Similarity 42.1%; Pred. NO. 0.042;
Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 6 LSSCCWGCSEISSLC 24
DB 6 LSNKCHIGCTKSLAKFC 24

RESULT 5

ID Q9N0T9 PRELIMINARY; PRT; 199 AA.
AC Q9N0T9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PREPRORELAXIN.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20191540; PubMed=10727251;
RA Hombach-Klonisch S., Abd-Elnaeim M., Skidmore J.A., Leiser R.,
RA Fischer B., Klonisch T.;
RT "Ruminant relaxin in the pregnant one-humped camel."
RL Biol. Reprod. 62:839-846(2000).
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR EMBL; AF254739; AAF67741.1; -.
DR HSP; P01348; 1RLX.
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR SMART; SM00078; IIGF; 1.
DR PROSITE; PS00262; INSULIN; 1.

RESULT 2
ID Q9TRG6 PRELIMINARY; PRT; 22 AA.
AC Q9TRG6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RELAXIN R-III A CHAIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RC MEDLINE=93257096; PubMed=8489740;
RA Kohsaka T., Takahara H., Sugawara K., Tagami S.;
RT "Endogenous heterogeneity of relaxin and sequence of the major form in pregnant sow ovaries."
RL Biol. Chem. Hoppe-Seyler 374:203-210(1993).
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR HSP; P01348; 1RLX.
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR PROSITE; PS00262; INSULIN; 1.
DR SEQUENCE 22 AA; 2527 MW; F4DB254222449313 CRC64;

Query Match 43.9%; Score 58; DB 6; Length 22;
Best Local Similarity 47.4%; Pred. NO. 0.018;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 LSSCCWGCSEISSLC 24
DB 4 LSEKCCQVCIRKDIARLC 22

RESULT 3

ID Q9MYK8 PRELIMINARY; PRT; 180 AA.
AC Q9MYK8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RELAXIN
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99115216; PubMed=9915995;
RA Klonisch T., Hombach-Klonisch S., Froehlich C., Kauffold J.,
RA Steger K., Huppertz B., Fischer B.;
RT "Nucleic acid sequence of feline preprorelaxin and its localization within the feline placenta."
RL Biol. Reprod. 60:305-311(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Hombach-Klonisch S., Klonisch T.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR EMBL; AF233688; AAF60303.1; -.
DR HSP; P04090; 6RLX.
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR SMART; SM00078; IIGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
DR SEQUENCE 180 AA; 20360 MW; 4C2CF371C698AF9F CRC64;

Query Match 43.2%; Score 57; DB 6; Length 180;

SQ SEQUENCE 199 AA; 22386 MW; F69BBD7E4F4A8089 CRC64;

Query Match 42.4%; Score 56; DB 6; Length 199;
Best Local Similarity 42.1%; Pred. No. 0.34;
Matches 8; Conservative 5; Mismatches 6; Indels

```
QY      6  LSSCCKWGCSKSEISLC  24
          |  ||: |||: |:|: |
Db     181  LGERCCQKGCSRKEMATAC  199
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RESULT	6	
Q920G7	PRELIMINARY;	129 AA.
ID		
AC	Q920G7;	
DT	01-DEC-2001 (TrEMBLrel. 19, Created)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
DE	CD59B.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_taxid=10090;	
RP	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=129/SV;	
RC	MEDLINE=21363798; PubMed=11471050;	
RA	Qin X., Miwa T., Aktas H., Gao M., Lee C., Qian Y.M., Morton C.C.,	
RA	Shahsafaei A., Song W.C., Halperin J.A.;	
RT	"Genomic structure, functional comparison, and tissue distribution of	
RT	mouse Cd59a and Cd59b.";	
RL	Mamm. Genome 12:582-589(2001).	
RL	EMBL; AF292401; AAL04434.1; -.	
SR	SEQUENCE 129 AA; 14226 MW;	
DR	3B80648C8C30CF635 CPC64.	

Query Match 39.8%; Score 52.5; DB 11; Length 129;
Best Local Similarity 37.5%; Pred. No. 0.8;
Matches 12; Conservative 5; Mismatches 4; Indels 11; Gaps 2;

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QY      3 LAGLSSSCKWG-CSK-----SEISSL 23
      :||: | ||: | :|
Db      79 VAGIOSKCCQWDLCKNKLGLGEEPNAETSSL 110

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RESULT	7
ID	Q28430
AC	PRELIMINARY;
DT	PRT; 24 AA.
DD	Q28430;
DE	01-NOV-1996 (TREMBLrel. 01, Created)
DE	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
RELX	RELAXIN (FRAGMENT).
GOS	RLX.
OOC	Gorilla gorilla (gorilla).
OOC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OOC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
NRN	NCBI_TaxID=9593;
RNP	[1]
RRP	SEQUENCE FROM N.A.
RRC	STRAIN=RG YK;
ERRA	Evans B.B.A., Fu P., Tregear G.G.W.;
ERRL	"Characterisation of primate relaxin genes.";
J. Mol. Endocrinol.	0:0(1993).
-1-	SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
EMBL:	-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
HSP:	EMBL; Z27228: CAA81742.1; -.
IPRO:	HSP; P04090: 6RLX.
PSO:	InterPro; IPR000739; Insulin_IGF_relaxin.
TER	PROSITE; PS00262; INSULIN; 1.
NON TER	1

SQ SEQUENCE 24 AA; 2673 MW; 5615D4B92C1DFD24 CRC64;

Query Match	39.4%	Score 52;	DB 6;	Length 24;
Best Local Similarity	33.3%	Pred. NO. 0.18;		
Matches	7;	Conservative	6;	Mismatches 8;
				Indels 0;
				Gaps 0;

```

QY      4  AGLSSCCCKWGCSKSEISLC  24
      : |::|| |::|::|
Db      4  SALANKCCHVGCTKRSLAREC  24

```

RESULT	8
Q28781	
ID	Q28781 PRELIMINARY; PRT; 24 AA.
AC	C28781;
DC	01-NOV-1996 (TReMBLrel. 01, Created)
DT	01-NOV-1996 (TReMBLrel. 01, last sequence update)
DD	01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE	RELAXIN (FRAGMENT).
DR	RLX.
OS	Pongo pygmaeus (Orangutan).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
OX	NCBM_Taxid=9600;
[1]	
RN	SEQUENCE FROM N.A.
RP	STRAIN-RG YK 287;
RC	Evans B.B.A., Fu P., Tregear G.G.W.;
RA	"Characterisation of primate relaxin genes.";
RT	J. Mol. Endocrinol. 0:0-0(1993).
CC	- - SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC	- - SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC	EMBLI; Z27229; CAA81743.1; -.
DR	HSSP; P04090; 6RLX.
DR	InterPro: IPR000739; Insulin_IGF_relaxin.
DR	PROSITE; PS00262; INSULIN; 1.
FT	NON_TER 1
SQ	SEQUENCE 24 AA; 2673 MW; 5615DA4B92C1DFD24 CRC64;

Query Match 39.4%; Score 52; DB 6; Length 24;
Best Local Similarity 33.3%; Pred. No. 0.18;
Matches 7; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

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QY      4 AGLSSCCKWGCSEISLC 24
      : | : | | | : | : |
Db      4 SALANKCCHVGCTKRSLAREC 24
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RESULT	9
Q9W1A5	
ID	PRELIMINARY; PRT; 868 AA.
AC	Q9W1A5;
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DD	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE	CG13569 PROTEIN.
DE	CG13569.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NB_I TaxID=727;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BERKELEY;
RCX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Beran B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fofler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ihegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003463; AAF47168.1;
 DR FlyBase; FBgn0034979; CG13569.
 DR InterPro; IPR001283; SCP.
 DR SMART; SM00198; SCP; 3.
 SQ SEQUENCE 868 AA; 98470 MW; 4EA194B97F240D0E CRC64;

Query Match 39.08; Score 51.5; DB 5; Length 868;
 Best Local Similarity 52.6%; Pred. No. 7.6;
 Matches 10; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 7 SSSCKGCKSKS-ETSSLC 24
 :||| :||| :||| :||| :|||
 Db 533 ASSCSGWTGTTKSKPANLC 551

RESULT 10
 Q9LV78 PRELIMINARY; PRT; 262 AA.
 ID Q9LV78
 AC Q9LV78
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
 DE GENOMIC DNA, CHROMOSOME 5, P1 CLONE:MXK3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
 RT clones."
 RL DNA Res. 7:31-63(2000).
 DR EMBL; AB019236; BAA97312.1; -.

SQ SEQUENCE 262 AA; 28098 MW; 5CD397647893BA11 CRC64;

Query Match 38.6%; Score 51; DB 10; Length 262;
 Best Local Similarity 47.6%; Pred. No. 2.8;
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 VLGLSSCKGCKSKSEISS 22
 :||| :||| :||| :||| :|||
 Db 121 VLGLSSCKGCKSKSEISS 141

RESULT 11
 Q95YP6 PRELIMINARY; PRT; 370 AA.
 ID Q95YP6
 AC Q95YP6
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE HYPOTHETICAL PREDICTED PROTEIN LM15-1.74, UNKNOWN FUNCTION.
 GN LM15-1.74.
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OC NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIDELIN;
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIDELIN;
 RX MEDLINE=98146435; PubMed=9477341;
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
 RA Smith D.F.;
 RT "A physical map of the Leishmania major Friedlin genome."
 RL Genome Res. 8:135-145(1998).
 DR EMBL; AL160371; CAC5905.1; -.
 SQ SEQUENCE 370 AA; 38847 MW; 328C7ED7A2174886 CRC64;

Query Match 38.6%; Score 51; DB 5; Length 370;
 Best Local Similarity 58.8%; Pred. No. 3.9;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 AGLSSCKGCKSKSEI 20
 :||| :||| :||| :||| :|||
 Db 326 AGLSSCKGCKSKSEI 342

RESULT 12
 Q9HYX0 PRELIMINARY; PRT; 1159 AA.
 ID Q9HYX0
 AC Q9HYX0
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE PROBABLE TWO-COMPONENT SENSOR.
 GN PA3271.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OC NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Huffnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.B., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;

RT *Complete genome sequence of Pseudomonas aeruginosa PAO1, an
 RL opportunistic pathogen.*;
 CC Nature 406:959-964(2000).
 CC -|- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
 CC REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
 CC -|- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
 DR EMBL; AE004749; AAG06659.1; -
 DR InterPro: IPR004358; BCTRSENSOR.
 DR InterPro: IPR003594; HATPase_c.
 DR InterPro: IPR003661; HIS_kinA.
 DR InterPro: IPR004359; HIS_kinA.
 DR InterPro: IPR001734; Na_solut_sympo.
 DR InterPro: IPR000014; PAS.
 DR InterPro: IPR001789; Response_reg.
 DR Pfam; PF02518; HATPase_c; 1.
 DR Pfam; PF00072; response_reg; 1.
 DR Pfam; PF00512; signal; 1.
 DR PRINTS; PR00344; BCTRSENSOR.
 DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00388; Hiska; 1.
 DR SMART; SM00091; PAS; 1.
 DR SMART; SM00448; REC; 1.
 DR PROSITE; PS0283; NA_SOLUT_SYMP_3; 1.
 KW Complete proteome; Kinase; Phosphorylation; Sensory transduction;
 KW Transference.
 SQ SEQUENCE 1159 AA; 127452 MW; 1C4D145CE0E190CF CRC64;

Query Match 38.6%; Score 51; DB 16; Length 1159;
 Best Local Similarity 35.7%; Pred. No. 12;
 Matches 10; Conservative 7; Mismatches 5; Indels 6; Gaps 1;

QY 2 VLAGLSSCCCKWGC-----SKSETSSL 23
 DB 1050 ILAGMNLSSRWGCQVWTARRECATL 1077

RESULT 13
 ID O62189 PRELIMINARY; PRT; 399 AA.
 AC O62189;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE F31B9.1 PROTEIN.
 GN F31B9.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Steward C.A.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99069613; PubMed-9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.*;
 RL Science 282:2012-2018(1998).
 RL EMBL; Z81520; CAB04223.1; -
 DR InterPro: IPR002106; AA_rRNA_ligase_II.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00339; AA_rRNA_LIGASE_II_2; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 SQ SEQUENCE 399 AA; 45577 MW; 83FF18CF47A7CF88 CRC64;

Query Match 37.9%; Score 50; DB 5; Length 399;
 Best Local Similarity 59.1%; Pred. No. 6.1;

Matches 13; Conservative 1; Mismatches 4; Indels 4; Gaps 2;
 QY 1 DVLAGLSSCCCKW---GCSKSE 19
 DB 343 DVAAGISSFCF-WLLPFSKSE 363
 RESULT 14
 Q23141
 ID Q23141 PRELIMINARY; PRT; 823 AA.
 AC Q23141;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 95.3 KDA PROTEIN.
 GN W03B1.2
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE-99069613; PubMed-9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.*;
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Miller N., Bradshaw H., Wu X., Gattung S.;
 RT "The sequence of C. elegans cosmid W03B1.*;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.*;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U58753; AAC24437.1; -
 DR InterPro: IPR002111; Cat_channel_TrpL.
 KW Hypothetical protein.
 SQ SEQUENCE 823 AA; 95286 MW; 5AC484962DCDD7D4 CRC64;

Query Match 37.9%; Score 50; DB 5; Length 823;
 Best Local Similarity 61.1%; Pred. No. 12;
 Matches 11; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 6 LSSSCCKGCKSKSEISSL 23
 DB 664 LITSGCCK--CSSTAISL 679

RESULT 15
 ID Q9LZV3 PRELIMINARY; PRT; 448 AA.
 AC Q9LZV3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE (1-4)-BETA-MANNAN ENDOHYDROLASE-LIKE PROTEIN.
 GN T20115.200.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Terry N., Ardiles W., Buysshaert C., Dasseville R.,
 RA De Clerck R., De Keyser A., Neyt P., Van Den Daele H.,

RA Villaroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W.,
 RA Rudd S., Lencke K., Mayer K.F.X.,
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases..
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL162351; CAB82763.1: -;
 DR InterPro: IPR000886; ER_target.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 KW Hydrolase.
 SQ SEQUENCE 448 AA; 50622 MW; 977B341312A54D7D CRC64;

Query Match 37.5%; Score 49.5; DB 10; Length 448;
 Best Local Similarity 41.7%; Pred. No. 8.2;
 Matches 10; Conservative 4; Mismatches 7; Indels 3; Gaps 1;

QY 3 LAGLSSSC--CKWGCSKSEISSL 23
 || :| | | | | :|
 Db 416 LAIFNSLCSWRCRWGCKKKNQTAL 439

Search completed: June 27, 2002, 16:16:31
 Job time: 500 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2002, 16:08:08 ; Search time 73.16 Seconds
(without alignments)
40.992 Million cell updates/sec

Title: US-09-781-077-2_COPY_26_52

Perfect score: 150

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Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	150	100.0	142	22	AA198114
2	87	58.0	40	17	AA196006
3	82	54.7	30	20	AA191963
4	82	54.7	31	21	AA195773
5	82	54.7	135	19	AA197925
6	82	54.7	135	20	AA191961
7	82	54.7	135	21	AA190173
8	82	54.7	135	21	AA192439
9	82	54.7	135	21	AA195770
10	82	54.7	135	21	AA198328
11	82	54.7	135	22	AA1924033

12	82	54.7	135	22	AA192309	Human PRO182 polyp
13	82	54.7	135	22	AA192310	Human immunostimul
14	82	54.7	135	22	AA192311	Human angioinogenesis
15	76	50.7	31	18	AA192312	Relaxin-like facto
16	75	50.0	135	19	AA192313	Mouse zins3 protei
17	75	50.0	135	21	AA192314	Mouse insulin fami
18	74	49.3	46	21	AA192315	Human Rlf partial
19	71	47.3	29	16	AA192316	Prorelaxin B-chain
20	71	47.3	29	16	AA192317	Human relaxin B-ch
21	71	47.3	46	11	AA192318	Ubiquitin C-termin
22	71	47.3	114	11	AA192319	Ubiquitin-relaxin
23	71	47.3	162	11	AA192320	H2 prorelaxin gene
24	71	47.3	162	11	AA192321	H2 prorelaxin dedu
25	71	47.3	185	5	AA192322	Sequence of human
26	71	47.3	185	5	AA192323	Sequence of human
27	71	47.3	185	5	AA192324	Amino acid sequenc
28	71	47.3	185	10	AA192325	Amino acid sequenc
29	71	47.3	185	10	AA192326	Angiotensin conver
30	71	47.3	220	22	AA192327	Asymmetry sequenc
31	69	46.0	33	17	AA192328	Relaxin analogue B
32	68	45.3	39	18	AA192329	Human relaxin part
33	66	44.0	46	21	AA192330	Relaxin B-chain.
34	64	42.7	52	16	AA192331	Sequence of porcine
35	55	36.7	182	4	AA192332	Sequence of porcine
36	55	36.7	182	5	AA192333	Human secreted pro
37	53	35.3	86	21	AA192334	Human gene 2 encod
38	53	35.3	86	22	AA192335	Caenorhabditis ele
39	53	35.3	106	21	AA192336	C. elegans insulin
40	53	35.3	106	21	AA192337	Human secreted pro
41	53	35.3	108	21	AA192338	Human gene 2 encod
42	53	35.3	108	22	AA192339	Prorelaxin fragme
43	53	35.3	150	16	AA192340	Human polypeptide
44	53	35.3	187	22	AA192341	Rat Zins2 testis-s
45	53	35.3	188	19	AA192342	

ALIGNMENTS

RESULT 1

AA192342

ID AA192342 standard; Protein; 142 AA.

XX AC

AA192342

XX DT

21-NOV-2001 (first entry)

XX DT

Human insulin homologue polypeptide Zins4.

XX DE

Human; insulin; zins4; relaxin; chromosome 19p13.11; cytostatic;

KW antifertility; vasotrophic; reproductive disorder; prostate disorder;

KW heart disorder; kidney disorder; gonadal development; pregnancy;

KW pubertal change; menopause; ovarian cancer; testicular cancer; ovulation;

KW polycystic ovarian syndrome; contractile tissue; cardiovascular disease;

KW birth control; impotence; myocyte; endothelial cell; osteoblast;

KW blood pressure; muscle tension; osmotic balance; gene therapy.

XX OS

Homo sapiens.

XX FH

Location/Qualifiers

FT Key

Peptide

1..25

/label= signal_peptide

FT Protein

26..142

/label= mature_protein

FT FT

/note= "Zins4, Claimed in claim 4"

FT Region

26..52

/label= B_chain

FT FT

/note= "Claimed in claim 1"

FT Region

34..47

/label= B_chain_consensus_sequence_region

FT FT

/note= "Given in SEQ ID NO 3"

FT Region

37..41

/label= B_chain_conserved_motif

FT /note= "Given in SEQ ID NO 5"
 FT Cleavage-site 53..54
 FT Region /label= C_peptide
 FT 55..118
 FT Region /label= C_peptide
 FT 55..114
 FT /note= "Claimed in claim 3"
 FT Cleavage-site 115..118
 FT /note= "Cleavage site at the junction of the C peptide
 FT and the A chain with a conserved RXR motif"
 FT 119..142
 FT Region /label= A_chain
 FT 128..142
 FT /note= "Claimed in claim 2"
 FT Region /label= A_chain_consensus_sequence_region
 FT /note= "Given in SEQ ID NO 4"
 FT
 XX WO200168862-A1.
 XX
 XX 20-SEP-2001.
 XX
 XX 09-FEB-2001; 2001WO-US04199.
 XX
 XX 10-MAR-2000; 2000US-0523346.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Holloway JL, Lok S, Jaspers SR;
 XX
 XX WPI; 2001-582454/65.
 XX
 XX N-PSDB; AAH79088.
 XX
 XX New insulin homologue polypeptide having homology to relaxin family,
 XX designated zins4 and zins4 polynucleotide, useful for diagnosing,
 XX preventing, treating reproductive, prostate, heart and kidney disorders
 XX
 XX Claim 6; Page 72-73; 79pp; English.
 XX
 XX The invention relates to an isolated insulin homologue zins4 having
 XX homology to the relaxin family. The zins4 gene, located on chromosome
 XX 19p13.11, encodes a 142 amino acid protein, where the zins4 polypeptide
 XX comprises a B chain and A chain comprising amino acid residues 26-52 and
 XX 119-142 respectively, joined by inter- and intra-chain disulfide bonds.
 XX zins4 has cytostatic, antifertility and vasotropic activity. zins4
 XX proteins are useful in applications for enhancing fertilisation during
 XX assisted reproduction in humans and animals and in therapies for treating
 XX reproductive disorders. zins4 protein is useful in treating reproductive,
 XX prostate, heart or kidney disorders and to identify cells, tissues or
 XX cell lines which respond to the zins4-stimulated pathway and to identify
 XX inhibitors of its activity. zins4 polypeptides and modulators of the
 XX polypeptide are useful in treating disorders associated with gonadal
 XX development, pregnancy, pubertal changes, menopause, ovarian cancer,
 XX prostate, testicular cancer, fertility, ovarian function, ovulation,
 XX polycystic ovarian syndrome and other reproductive functions including
 XX pathological conditions in ovary. Detection of zins4 polypeptides in the
 XX serum or tissue biopsy of a patient is useful for diagnosing ovarian
 XX cancer. The molecules are also useful for treating dysfunction associated
 XX with contractile tissues or to suppress or enhance contractility in vivo,
 XX treating cardiovascular disease, infertility, in vitro fertilization,
 XX birth control, treating impotence or other male reproductive dysfunction,
 XX inducing birth, for promoting growth, differentiation, development and/or
 XX maturation of ovarian cells, myocytes, endothelial cells, osteoblasts in
 XX culture and in the study of the ovarian cycle, reproductive function,
 XX ovarian cell-cell interactions and fertilisation. The polypeptide is also
 XX useful as a modulator of blood pressure, muscle tension and osmotic
 XX balance. The zins4 polynucleotide is useful in gene therapy.

Sequence 142 AA;

Query Match 100.0%; Score 150; DB 22; Length 142;
 Best Local Similarity 100.0%; Pred. No. 6.3e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAAPYGVRLCGREFIRAVIFTCGGSRW 27
 Db 26 raapvgrlcrrefiraviftcggsrw 52
 |||||

RESULT 2
 AAR96006
 ID AAR96006 standard; peptide; 40 AA.

XX AAR96006;
 AC AAR96006;
 DT 19-FEB-1997 (first entry)
 XX
 DE Asymmetry sequence #8.
 XX

KW Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;
 KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;
 KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;
 KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
 KW virus.

OS Synthetic.

XX WO9617956-A2.

XX 13-JUN-1996.

XX 07-DEC-1995; 95WO-US15944.

XX 09-DEC-1994; 94US-0353476.

XX (GENE-) GENE POOL INC.

XX Weininger AM, Weininger S;

XX WPI; 1996-287199/29.

XX Probe nucleic acids, target binding assemblies, etc - for detection
 XX and localisation of specific nucleic acid sequences, esp. HIV and
 XX HPV

XX Claim 21; Page 108-109; 172pp; English.

XX AAR95999-R96006 represent the asymmetry sequences of target binding
 XX assemblies (TBA) of the invention. The TBA is recognised by the target
 XX binding region (TBR) of a probe of the invention. The probe of the
 XX invention contains a TBR, a booster binding region (BBR), and an
 XX optional support or attachment (OSA). The TBA contains at least one
 XX nucleic acid recognition unit (NAR), and optionally a linker sequence, an
 XX assembly sequence, an asymmetry sequence, a nuclear localisation signal
 XX sequence, and an OSA. The assembly sequence and asymmetry sequences are
 XX responsible for the folding and association of the NARs. The NARs are
 XX selected from NF-kappa-B, SP1, TATA, human papillomavirus (HPV) E2, HPV
 XX LTR, human immunodeficiency virus (HIV) LTR and Tat binding units.
 XX linker sequence is an oligopeptide, which does not interfere with NAR
 XX function, but provides stability and control over the spacing of the NAR
 XX from the rest of the TBA. The OSA is an attached support or indicator,
 XX or other means of localisation of the probe. The probe can be used in a
 XX method for detecting or localising a specific target nucleic acid
 XX of sequence (TNA). The method is highly sensitive, and has a high degree
 XX of specificity. The method can be used for detecting specific nucleic
 XX acid sequences, including those found in human cells, in HIV, HPV, and
 XX other nucleic acid containing systems, including bacteria and viruses.

Sequence 40 AA;

Query Match 58.0%; Score 87; DB 17; Length 40;
 Best Local Similarity 70.0%; Pred. No. 1.9e-05;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVIFTCGGSRW 27

Db 9 rlcgrdlirafylcggrtw 28
 |||||: ||| |: |||: ||

RESULT 3
 AAY01963
 ID AAY01963 standard; Peptide; 30 AA.

XX AC AAY01963;
 XX DT 01-JUL-1999 (first entry)
 XX DE Insulin-like peptide (pro-ILP) chain B peptide.
 XX KW Insulin-like polypeptide; pro-ILP; ILP; insulin/IGF family;
 KW A chain; B chain; C chain; neurophysiological function;
 KW fluid homeostasis; electrolyte homeostasis; cardiovascular function;
 KW blood pressure; somatic; cardiac ionotropic activity;
 KW cardiac chronotropic activity; collagen deposition.

XX OS Homo sapiens.
 XX PN WO9915664-A1.
 XX PD 01-APR-1999.

XX PF 28-AUG-1998; 98WO-US17888.
 XX PR 24-SEP-1997; 97US-0059836.
 XX PA (GETH) GENENTECH INC.

XX PI Gurney A;

XX DR WPI; 1999-254713/21.
 XX N-PSDB; AAX35207.

XX PT Colon and uterus expressed insulin-like polypeptide, useful in the
 PT treatment of disorders related to neurophysiological function
 XX PS Claim 7; Page -: 75pp; English.

XX CC The present sequence represents insulin-like polypeptide (pro-ILP)
 CC chain B peptide. The ILP protein is expressed in the colon and uterus,
 CC and is a member of the insulin/IGF family. The immature pro-ILP
 CC comprises a 135 amino acid sequence, which is processed into the mature
 CC form which comprises an A chain and a B chain linked by disulfide bonds.
 CC The C-peptide of pro-ILP exists as a separate peptide after processing
 CC of pro-ILP. The ILP protein is useful in treatment of disorders related
 CC to neurophysiological function affecting fluid homeostasis, electrolyte
 CC homeostasis, cardiovascular function, blood pressure, somatic or cardiac
 CC ionotropic activity, cardiac chronotropic activity and collagen
 CC deposition. The methods can be used for diagnosing a physiologic or
 CC pathologic condition of the uterus, colon or other ILP-expressing cell
 CC or tissue and for diagnosis and screening of modulators and therapeutics.
 CC note: the present sequence does not appear in the specification; it was
 CC created using information provided.

XX SQ Sequence 30 AA;

Query Match 54.7%; Score 82; DB 20; Length 30;
 Best Local Similarity 66.7%; Pred. No. 7.5e-05;
 Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 7 VRLCGREFIRAVIFTCGSRW 27
 |||||: ||| |: |||: ||
 Db 8 vrlcgleyirtviycassrw 28

RESULT 4
 AAY95773
 ID AAY95773 standard; Peptide; 31 AA.

XX AC AAY95773;
 XX DT 07-NOV-2000 (first entry)

XX DE Human zins3 B chain peptide immunogen.
 XX KW zins3; insulin; relaxin; human; diagnosis; NIIDM;
 KW non-insulin dependent diabetes mellitus; immunogen.

XX OS Homo sapiens.
 XX PN WO200047776-A2.
 XX PD 17-AUG-2000.

XX PF 10-FEB-2000; 2000WO-US03515.
 XX PR 12-FEB-1999; 99US-0198248.
 XX PR 12-FEB-1999; 99US-0250125.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Jaspers SR, Whitmore TE, Conklin DC, Lofton-Day CE, Lok S;
 XX DR WPI; 2000-558220/51.

XX PT Identifying mutations in human chromosome lp31, preferably a zins3 gene
 PT mutation, comprises using an insulin/relaxin family member (designated
 PT zins3), useful for diagnosing non-insulin dependent diabetes -

XX PS Example 5; Page 34; 51pp; English.

XX CC The present sequence is that of a peptide from the B chain of
 CC human zins3 (see AAY95770). The peptide was used to immunize guinea
 CC pigs, rabbits and chickens to generate antibodies for zins3, which
 CC were used in assays to determine the tissue distribution and cell
 CC expression of zins3. zins3 is a novel member of the insulin/relaxin
 CC family whose gene maps to a region of human chromosome lp associated
 CC with non-insulin dependent diabetes mellitus (NIDDM). zins3
 CC polynucleotides and polypeptides can be used to diagnose disorders
 CC associated with abnormal expression of zins3, and to identify
 CC polymorphisms that result from mutations in the zins3 gene. The
 CC invention provides methods for identifying abnormalities in
 CC expression that are a factor in causing, or predisposing, a person
 CC to some defect in glucose metabolism, such as NIDDM.

XX SQ Sequence 31 AA;

Query Match 54.7%; Score 82; DB 21; Length 31;
 Best Local Similarity 66.7%; Pred. No. 7.8e-05;
 Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 7 VRLCGREFIRAVIFTCGSRW 27
 |||||: ||| |: |||: ||
 Db 8 vrlcgleyirtviycassrw 28

RESULT 5
 AAW37925
 ID AAW37925 standard; Protein; 135 AA.

XX AC AAW37925;

XX DT 01-SEP-1998 (first entry)

XX DE Human zins3 protein.

XX KW Insulin homologue; identification; isolation; zins3 receptor;
 KW treatment; disease; pre-elampsia; premature labour; Human.
 XX OS Homo sapiens.

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XX Key Location/Qualifiers
FH Peptide 23..48 "B chain"
FT /note="B chain"
FT Peptide 49..114
FT /note="C-peptide"
FT Peptide 115..135
FT /note="A chain"
XX WO9816635-A1.
XX PN
XX PD
XX PF 23-APR-1998.
XX PR 15-OCT-1997; 97WO-US18593.
XX PA 15-OCT-1996; 96US-0028177.
XX (ZYMO ) ZYMOGENETICS INC.
XX Conklin DC, Jaspers SR, Lofton-Day CE, Lok S;
XX WPI; 1998-251285/22.
XX N-PSDB; AAV29150.
XX Insulin homologue polypeptide(s) and antagonists - used to, e.g.
XX treat pre-eclampsia, premature labour and Crohn's disease.
XX Claim 2; Page 64-65; 81pp; English.
XX The zins3 protein is an insulin homologue protein. Polynucleotide
XX molecules taken from its gene can be introduced into a cultured cell
XX using an expression vector. The cell will express an insulin homologue
XX polypeptide encoded by the polynucleotide. The polypeptides can also be
XX expressed by introducing the polynucleotides into the germline of a
XX nonhuman animal. The polypeptides can be used to identify and isolate
XX receptors for zins3. Antibodies and antagonists of the polypeptides can
XX be used for treating disease associated with extracellular matrix and
XX vessels. The antibodies may also be used in the diagnosis of diseases
XX associated with the polypeptide, such as reproductive disorders
XX associated with the placenta and uterus, gastrointestinal diseases, and
XX placental and colon pathology. Antagonists against the polypeptide may
XX also be used to treat diseases such as preclampsia, premature labour, and
XX Crohn's disease.
XX Sequence 135 AA;

Query Match 54.7%; Score 82; DB 19; Length 135;
Best Local Similarity 66.7%; Pred. No. 0.00034;
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
DB 26 vrlcgleyirtviycasrw 46

RESULT 6
AAV01961
ID AAV01961 standard; Protein; 135 AA.
XX AC AAV01961;
XX 01-JUL-1999 (first entry)
XX DE
XX Pro-insulin-like peptide (pro-ILP).
XX Insulin-like polypeptide; pro-ILP; ILP; insulin/IGF family;
XX A chain; B chain; C chain; neurophysiological function;
XX fluid homeostasis; electrolyte homeostasis; cardiovascular function;
XX blood pressure; somatic; cardiac ionotropic activity;
XX cardiac chronotropic activity; collagen deposition.
XX OS Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..18
FT /label= Signal peptide
FT Modified-site 3..9
FT /note= "N-myristoylation site"
FT Modified-site 52..58
FT /note= "N-myristoylation site"

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XX WO9915664-A1.
XX PN
XX PD
XX PF 01-APR-1999.
XX PR 28-AUG-1998; 98WO-US17888.
XX PR 24-SEP-1997; 97US-0059836.
XX (GETH ) GENENTECH INC.
XX Gurney A;
XX WPI; 1999-254713/21.
XX N-PSDB; AAX35204.
XX Colon and uterus expressed insulin-like polypeptide, useful in the
XX treatment of disorders related to neurophysiological function
XX Claim 5; Fig 6B; 75pp; English.
XX The present sequence represents an insulin-like polypeptide (pro-ILP).
XX The protein is expressed in the colon and uterus, and is a member
XX of the insulin/IGF family. The immature pro-ILP comprises a 135 amino
XX acid sequence, which is processed into the mature form which comprises
XX an A chain and a B chain linked by disulfide bonds. The C-peptide of
XX pro-ILP exists as a separate peptide after processing of pro-ILP. The
XX ILP protein is useful in treatment of disorders related to
XX neurophysiological function affecting fluid homeostasis, electrolyte
XX homeostasis, cardiovascular function, blood pressure, somatic or cardiac
XX ionotropic activity, cardiac chronotropic activity and collagen
XX deposition. The methods can be used for diagnosing a physiologic or
XX pathologic condition of the uterus, colon or other ILP-expressing cell
XX or tissue and for diagnosis and screening of modulators and therapeutics.
XX Sequence 135 AA;

Query Match 54.7%; Score 82; DB 20; Length 135;
Best Local Similarity 66.7%; Pred. No. 0.00034;
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
DB 26 vrlcgleyirtviycasrw 46

RESULT 7
AAB00173
ID AAB00173 standard; Protein; 135 AA.
XX AC AAB00173;
XX 08-FEB-2001 (first entry)
XX DE
XX PRO182 polypeptide.
XX PRO211; PRO228; PRO538; PRO172; PRO182; neoplasia; inhibition;
XX tumour; treatment; therapy; agonist; antibody; breast cancer;
XX ovarian cancer; renal cancer; colorectal cancer; uterine cancer;
XX prostate cancer; lung cancer; bladder cancer; melanoma; leukaemia;
XX inflammatory disorder; angiogenic disorder; immunologic disorder;
XX human.
XX OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..18
FT /label= Signal peptide
FT Modified-site 3..9
FT /note= "N-myristoylation site"
FT Modified-site 52..58
FT /note= "N-myristoylation site"

```


FT Modified-site 88..92 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 96..102 /note= "N-myristoylation site"
 FT Modified-site 107..111 /note= "cAMP- and cGMP-dependent protein kinase"
 FT Modified-site 113..117 /note= "Casein kinase II phosphorylation site"
 FT Domain 121..136 /label= Insulin family signature
 FT Modified-site 125..131 /note= "N-myristoylation site"
 FT Modified-site 127..131 /note= "Casein kinase II phosphorylation site"
 XX
 PN WO200055319-A1.
 XX
 PN 21-SEP-2000.
 PD
 PD 02-DEC-1999; 99WO-US28564.
 XX
 XX 12-MAR-1999; 99US-0123957.
 PR 28-APR-1999; 99US-0131445.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 08-SEP-1999; 99WO-US20594.
 PR 15-SEP-1999; 99WO-US21090.
 PR 05-OCT-1999; 99WO-US23089.
 PR 30-NOV-1999; 99WO-US28313.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, Wood WT;
 PI Yuan J;
 XX
 DR WPI; 2000-638201/61.
 DR N-PSDB; AAA54109.
 XX
 XX PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for
 PT treating tumors including cancers of the breast and lung,
 PT leukemia and for identifying compounds capable of inhibiting
 PT growth of neoplastic cells
 XX
 PS Claim 31; Fig 10; 133pp; English.
 XX
 CC Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides
 CC or their agonists (preferably anti-PRO agonist antibody or a small
 CC molecule mimicking the biological activity of PRO polypeptide) are
 CC useful in vitro or in vivo for inhibiting the growth of a tumour cell.
 CC Compositions comprising the PRO polypeptides are useful for
 CC inhibiting neoplastic cell growth and for treating cancer including
 CC breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder,
 CC central nervous system cancer, melanoma and leukemia in a mammal.
 CC The PRO polypeptides are also useful for treating other disorders
 CC such as neuronal, glial, astrocytal, hypothalamic and other glandular,
 CC macrophagal, epithelial, stromal, blastocelial disorders and
 CC inflammatory, angiogenic and immunologic disorders as well as being
 CC useful for identifying agonists to PRO polypeptides by contacting the
 CC polypeptide with a candidate molecule and monitoring biological
 CC activity mediated by the polypeptide.
 XX
 SQ Sequence 135 AA;

Query Match 54.7%; Score 82; DB 21; Length 135;
 Best Local Similarity 66.7%; Pred. No. 0.00034;
 Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 7 VRLCGREFIRAVITTCGSRW 27
 ||||| 1:1 ||: | ||
 Db 26 vrlcglylrvtyivycassrw 46

RESULT 8
 AAB24391
 ID AAB24391 standard; Protein; 135 AA.
 XX
 AC AAB24391;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Human PRO182 protein sequence SEQ ID NO:16.
 XX
 KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
 KW cytosstatic; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO200032221-A2.
 XX
 PD 08-JUN-2000.
 XX
 XX 30-NOV-1999; 99WO-US28313.
 XX
 PR 01-DEC-1998; 98WO-US25108.
 PR 16-DEC-1998; 98US-0112850.
 PR 12-JAN-1999; 99US-0115554.
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-OCT-1999; 99US-0162506.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
 PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
 PI Watanabe CK, Williams PM, Wood WT;
 XX
 DR WPI; 2000-412154/35.
 DR N-PSDB; AAA77521.
 XX
 XX Nucleic acids encoding PRO polypeptides useful for preventing,
 PT diagnosing and treating a cardiovascular, endothelial or
 PT angiogenic disorders in mammals -
 XX
 PS Claim 72; Fig 8; 315pp; English.
 XX
 XX The present invention describes nucleic acids encoding PRO polypeptides
 CC useful for preventing, diagnosing and treating a
 CC cardiovascular, endothelial or angiogenic disorder in mammals by
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,
 CC and for identifying agonists and antagonists of these processes. The
 CC nucleic acids and the proteins they encode may be used in the
 CC prevention, treatment and diagnosis of diseases associated with
 CC inappropriate PRO expression such as cardiovascular, endothelial or
 CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
 CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors
 CC containing them and the PRO polypeptide may be used to treat disorders
 CC associated with decreased PRO expression. AAA77510 to AAA77721 and
 CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 135 AA;

Query Match 54.7%; Score 82; DB 21; Length 135;
Best Local Similarity 66.7%; Pred. No. 0.00034;
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVITCGGSRW 27
| | | | | : | | | | : | | | |
Db 26 vrlcglevrtviycassrw 46

RESULT 9

ID AAY95770 standard; Protein; 135 AA.

AC AAY95770;

XX 07-NOV-2000 (first entry)

XX Human insulin family homologue zins3.

XX Zins3; insulin; relaxin; human; diagnosis; NIIDM;
KW non-insulin dependent diabetes mellitus.

XX Homo sapiens.

XX Location/Qualifiers

FT Peptide 1..22

FT /label= Signal_peptide

FT Peptide 23..48

FT /label= B-chain

FT Peptide 49..114

FT /label= C-chain

FT Peptide 115..135

FT /label= A-chain

XX WO200047776-A2.

XX 17-AUG-2000.

XX 10-FEB-2000; 2000WO-US03515.

XX 12-FEB-1999; 99US-0198248.

XX 12-FEB-1999; 99US-0250125.

XX (ZYMO) ZYMOGENETICS INC.

XX Jaspers SR, Whitmore TE, Conklin DC, Lofton-Day CE, Lok S;

XX WPI; 2000-558220/51.

XX N-PSDB; AAA50150.

XX Identifying mutations in human chromosome 1p31, preferably a zins3 gene

XX mutation, comprises using an insulin/relaxin family member (designated

XX zins3), useful for diagnosing non-insulin dependent diabetes

XX Claim 2; Page 44-45; 51pp; English.

XX The present sequence is that of zins3, a novel member of the

XX insulin/relaxin family. The zins3 gene maps to human chromosome

XX 1p31, a region that is correlated to a heritable form of non-insulin

XX dependent diabetes mellitus (NIIDM). zins3 mRNA is not expressed

XX in detectable amounts in healthy tissue, indicating that the zins3

XX polynucleotide is a candidate marker for a disease state and/or a

XX specialized cell type. zins3 polynucleotides and polypeptides can

XX be used to diagnose disorders associated with abnormal expression

CC members of the insulin family, cleavage at the C-terminus of the
CC B-chain and at the N-terminus of the A-chain, resulting in
CC removal of the C-peptide. Cysteine residues at positions 29 and 41
CC (B-chain) and 121 and 135 (A-chain) are capable of associating
CC through cysteine bridges and forming disulfide-bonded molecules.
XX

SQ Sequence 135 AA;

Query Match 54.7%; Score 82; DB 21; Length 135;

Best Local Similarity 66.7%; Pred. No. 0.00034;

Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVITCGGSRW 27

Db 26 vrlcglevrtviycassrw 46

RESULT 10

AAY83228

ID AAY83228 standard; Protein; 135 AA.

XX AAY83228;

XX 16-AUG-2000 (first entry)

XX PRO182 Polypeptide.

XX Inhibition; cancer; neoplasia; tumour; breast; ovary; renal;

KW colorectal; uterus; prostate; lung; bladder; central nervous system;

KW CNS; melanoma; leukaemia; PRO211; PRO228; PRO538; PRO172; PRO182;

XX human.

XX Homo sapiens.

XX Location/Qualifiers

FT Peptide 1..18

FT /label= Signal_peptide

FT Modified-site 3..9

FT /note= "N-myristoylation site"

FT Modified-site 52..58

FT /note= "N-myristoylation site"

FT Modified-site 88..92

FT /note= "Casein kinase II phosphorylation site"

FT Modified-site 96..102

FT /note= "N-myristoylation site"

FT Modified-site 107..111

FT /note= "cAMP and cGMP dependent protein kinase phosphorylation site"

FT Modified-site 113..117

FT /note= "Casein kinase II phosphorylation site"

FT Region 121..136

FT /note= "Insulin family signature sequence"

FT Modified-site 125..131

FT /note= "N-myristoylation site"

FT Modified-site 127..131

FT /note= "Casein kinase II phosphorylation site"

XX WO200021996-A2.

XX 20-APR-2000.

XX 05-OCT-1999; 99WO-US23089.

XX 13-OCT-1998; 98US-0104080.

XX (GETH) GENENTECH INC.

XX Ashkenazi A, Goddard A, Gurney AL, Klein RD, Napier M, Wood WT;
PI Yuan J;
XX WPI; 2000-317943/27.
DR N-PSDB; AA293704.

XX Composition for inhibiting neoplastic cell growth and treating cancers
PT of ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228,
PT PRO538, PRO172 or PRO182 polypeptide or their agonist
XX

PS Claim 14; Figure 10; 122pp; English.

XX Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182
CC polypeptide or their agonists, mixed with a carrier is useful for
CC inhibiting neoplastic growth and treating tumors such as cancers of
CC breast, ovary, renal, colorectal, uterus, prostate, lung, bladder,
CC central nervous system, melanoma and leukaemia.
XX

SQ Sequence 135 AA;

Query Match 54.7%; Score 82; DB 21; Length 135;
Best Local Similarity 66.7%; Pred. No. 0.00034;
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVIFTCGSRW 27
||||| I:|:| I:|:| I:|:|
Db 26 vrlcgleiyrtviycassrw 46

RESULT 11

AAM24033
ID AAM24033 standard; Protein; 135 AA.

AC AAM24033;

DT 12-OCT-2001 (first entry)

DE Human EST encoded protein SEQ ID NO: 1558.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition.

OS Homo sapiens.

PN WO200154477-A2.

XX 02-AUG-2001.

PF 25-JAN-2001; 2001WO-US02687.

PR 25-JAN-2000; 2000US-0491404.

PR 17-JUL-2000; 2000US-0617746.

PR 03-AUG-2000; 2000US-0631451.

PR 15-SEP-2000; 2000US-0663870.

PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;

DR WPI; 2001-476164/51.

XX N-PSDB; AAH98692.

PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -

PS Claim 20; Page 1068-1069; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a

CC protein of the invention.
XX
SQ Sequence 135 AA;

Query Match 54.7%; Score 82; DB 22; Length 135;
Best Local Similarity 66.7%; Pred. No. 0.00034;
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVIFTCGSRW 27
||||| I:|:| I:|:| I:|:|
Db 26 vrlcgleiyrtviycassrw 46

RESULT 12

AAU12309
ID AAU12309 standard; Protein; 135 AA.

AC AAU12309;

DT 24-OCT-2001 (first entry)

XX Human PRO182 polypeptide sequence.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy.

OS Homo sapiens.

PN WO200140466-A2.

XX 07-JUN-2001.

PF 01-DEC-2000; 2000WO-US32678.

PR 01-DEC-1999; 99WO-US28301.

PR 02-DEC-1999; 99WO-US28334.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 09-DEC-1999; 99US-0170262.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 30-DEC-1999; 99WO-US30999.

PR 06-JAN-2000; 2000WO-US00277.

PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PR 01-MAR-2000; 2000WO-US05601.

PR 20-MAR-2000; 2000WO-US07377.

PR 21-MAR-2000; 2000WO-US07532.

PR 30-MAR-2000; 2000WO-US08439.

PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.

PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.

PR 10-NOV-2000; 2000WO-US30873.

XX (GETH) GENENTECH INC.

XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;

PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;

XX WPI; 2001-408281/43.

DR N-PSDB; AAS21381.

XX Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical -
 XX
 PS Claim 12; Fig 276; 813pp; English.
 XX
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX
 CC Sequence 135 AA;

Query Match 54.7%; Score 82; DB 22; Length 135;
 Best Local Similarity 66.7%; Pred. No. 0.00034;
 Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 7 VRLCGREFIRAVFTCGGSRW 27

Db 26 vrlcgleyirtviycassrw 46

RESULT 13

ID AAB20110 standard; Protein; 135 AA.

AC AAB20110;

XX 30-APR-2001 (first entry)

XX Human immunostimulant PRO182.

XX PRO182; UNQ156; human; immune disease; autoimmune disease;
 KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;
 KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;
 KW hepatotropic; virucide; dermatological; antipsoriatic;
 KW antiasthmatic; antiallergic; immunostimulant.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..18

FT Protein /label= Signal_peptide

FT /label= Mature_protein

FT Modified-site 107..111

FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"

FT Modified-site 3..9

FT /note= "N-myristoylation site"

FT Modified-site 52..58

FT /note= "N-myristoylation site"

FT Modified-site 96..102

FT /note= "N-myristoylation site"

FT Modified-site 125..131
 FT /note= "N-myristoylation site"
 FT Peptide 121..136
 FT /note= "insulin family signature"

XX WO200105972-A1.

XX 25-JAN-2001.

XX 15-MAR-2000; 2000WO-US06884.

XX 20-JUL-1999; 99US-0144758.

XX (GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;
 PI Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;
 PI Wood WI;

XX WPI; 2001-103149/11.

XX N-PSDB; AAF30052.

XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for
 PT diagnosing and treating immune-related disorders, such as multiple
 PT sclerosis, rheumatoid arthritis and diabetes -

PS Claim 20; Fig 6; 127pp; English.

XX The present sequence is that of PRO182 (UNQ156), a novel human
 CC immunomodulator protein encoded by cDNA (see AAF30052) isolated
 CC from a uterine cDNA library. The invention provides polynucleotides
 CC (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20)
 CC including PRO182. Claimed compositions comprising these proteins or
 CC their agonists are useful for increasing infiltration of inflammatory
 CC cells into a tissue of a mammal, stimulating or enhancing an immune
 CC response in a mammal, or increasing the proliferation of T-lymphocytes
 CC in a mammal in response to an antigen. Claimed compositions
 CC comprising the PRO polypeptide or its antagonist have the opposite
 CC effect. A claimed method for treating an immune related disorder,
 CC such as a T cell disorder, involves administering the PRO polypeptide,
 CC an agonist antibody or an antagonist antibody. The disorder is
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathy,
 CC systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC multiple sclerosis), autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease (ulcerative colitis and Crohn's disease),
 CC gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated
 CC skin diseases (such as bullous skin disease, erythema multiforme and
 CC psoriasis), allergic diseases (such as asthma, allergic rhinitis,
 CC atopic dermatitis, food hypersensitivity and urticaria), immunologic
 CC diseases of the lung and transplantation associated diseases (such
 CC as graft rejection and graft-versus-host disease) (all claimed).

XX Claimed methods of diagnosing these disorders comprise detecting
 CC the level of expression of the PRO gene. Also claimed are a method
 CC of identifying a compound capable of inhibiting the expression or
 CC activity of the PRO polypeptide, vectors, host cells and
 CC antibodies.

XX Sequence 135 AA;

Query Match 54.7%; Score 82; DB 22; Length 135;
 Best Local Similarity 66.7%; Pred. No. 0.00034;
 Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27

Db 26 vrlcgleyirtviycassrw 46

RESULT 14

AAB53072
 ID AAB53072 standard; Protein; 135 AA.
 AC AAB53072;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Human angiogenesis-associated protein PRO182, SEQ ID NO:41.
 XX
 KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal.
 XX

OS Homo sapiens.
 XX

PN WO200053753-A2.
 XX

PD 14-SEP-2000.
 XX

PF 05-JAN-2000; 2000WO-US00219.
 XX

PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 14-MAY-1999; 99US-0134287.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20534.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 02-DEC-1999; 99WO-US28584.
 PR 02-DEC-1999; 99WO-US28565.
 XX

PA (GETH) GENENTECH INC.
 XX

PI Ashkenazi AJ, Baker KP, Ferrata N, Gerber H, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
 XX

DR WPI; 2001-090793/10.
 DR N-PSDB; AAC97396.
 XX

PT New isolated nucleic acid for producing a PRO polypeptide, analyzing
 PT genetic disorders and treating cardiovascular, endothelial or
 PT angiogenic disorders, such as atherosclerosis, wounds or cancer -
 XX

PS Claim 69; Fig 18; 293pp; English.
 XX

CC The invention relates to novel human angiogenesis-associated proteins
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
 CC PRO proteins. The invention also relates to vectors and host cells
 CC comprising a PRO nucleic acid, the recombinant production of a PRO
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
 CC compounds which inhibit the expression of a PRO gene. The invention
 CC additionally encompasses methods of identifying modulators of PRO
 CC expression or activity; diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting
 CC mutations in a PRO gene, or the expression level of a PRO gene within a
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a

CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
 CC administration of a PRO protein, or an agonist or antagonist thereof.
 CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
 CC agonists and PRO antagonists may be used as therapeutic agents to treat
 CC cardiovascular, endothelial or angiogenic disorders, such as
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
 CC disease, or stroke. PRO nucleic acids are additionally useful in the
 CC recombinant production of PRO proteins, as hybridisation probes to
 CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,
 CC to map genes encoding PRO proteins, to analyse genetic disorders, and in
 CC gene therapy. PRO nucleic acids can also be used to produce transgenic
 CC animals useful for the development and screening of potential
 CC therapeutic agents. The present sequence represents a PRO protein of the
 XX invention.

SQ Sequence 135 AA;

Query Match 54.7%; Score 82; DB 22; Length 135;

Best Local Similarity 66.7%; Pred. No. 0.00034;

Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVITCGGSRW 27

||||| :||| :| :|||

Db 26 vrlcgleiyrtviycassrw 46

RESULT 15

AABW07863

ID AABW07863 standard; peptide; 31 AA.

XX AC AABW07863;

XX 27-AUG-1997 (first entry)

XX Relaxin-like factor B chain.

XX A chain; B chain; relaxin-like factor; RLF; relaxin;

KW cardiovascular disease; neurodegenerative disease;

KW neurological disease; sinus bradycardia; depression; hair loss;

KW collagen; scleroderma; fibronectin; insulin.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Disulfide-bond 10

FT Disulfide-bond 22 /note= "Forms disulphide bond with A chain Cys11"

FT Disulfide-bond 22 /note= "Forms disulphide bond with A chain Cys24"

XX W09640186-A1.

XX 19-DEC-1996.

XX 16-MAY-1996; 96WO-US07399.

XX 07-JUN-1995; 95US-0484219.

XX (CONN-) CONNECTIVE THERAPEUTICS INC.

XX (UYSC-) UNIV SOUTH CAROLINA.

XX Schwaab C, Unemori E;

XX WPI; 1997-051882/05.

XX Relaxin-like factor - useful as replacement for relaxin in treatment

PT of, e.g. cardiovascular or neurodegenerative disease

XX Claim 1; Page 48; 60pp; English.

XX

CC The sequences given in AAW07862-63 represent the A and B chains of
 CC relaxin-like factor (RLF). RLF displaces bound relaxin tracer from
 CC the receptor to which it is bound. The RLF can be used to treat
 CC relaxin treatable conditions, esp. cardiovascular disease, neuro-
 CC degenerative or neurological disease, sinus bradycardia, depression,
 CC hair loss or diseases related to uncontrolled or abnormal formation of
 CC collagen (e.g. scleroderma) or fibronectin. RLF can be radiolabelled
 CC for use in binding assays, and for relaxin receptor mapping. RLF
 CC shares primary and secondary homology to relaxin and insulin.

XX Sequence 31 AA;

Query Match 50.7%; Score 76; DB 18; Length 31;
 Best Local Similarity 55.0%; Pred. No. 0.00056;
 Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLCGRFIRAVIFTCGSRW 27

Db 8 klcghivralrvvcgprw 27

Search completed: June 27, 2002, 16:08:09
 Job time: 278 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2002, 16:08:44 ; Search time 28,78 Seconds
(without alignments)
22,915 Million cell updates/sec

Title: US-09-781-077-2_COPY_26_52
Perfect score: 150
Sequence: 1 RAAPYGVRLCGREFIRAVITCGSRW 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	116	77.3	30	6	5464756-16 Patent No. 5464756
2	102	68.0	29	6	5464756-15 Patent No. 5464756
3	87	58.0	40	2	US-08-353-476-92 Sequence 92, Appl
4	82	54.7	135	3	US-08-950-720A-2 Sequence 2, Appl
5	76	50.7	31	2	US-08-484-219-4 Sequence 4, Appl
6	76	50.7	101	3	US-08-950-720A-14 Sequence 14, Appl
7	75	50.0	135	3	US-08-950-720A-6 Sequence 6, Appl
8	71	47.3	29	1	US-08-443-568B-2 Sequence 2, Appl
9	71	47.3	29	2	US-08-484-219-5 Sequence 5, Appl
10	71	47.3	32	5	PCT-US94-06997-2 Sequence 5, Appl
11	71	47.3	33	6	5464756-11 Patent No. 5464756
12	71	47.3	33	6	5464756-10 Patent No. 5464756
13	71	47.3	52	1	US-08-443-568B-14 Sequence 14, Appl
14	71	47.3	52	5	PCT-US94-06997-14 Sequence 14, Appl
15	71	47.3	77	1	US-08-443-568B-10 Patent No. 5464756
16	71	47.3	77	1	PCT-US94-06997-10 Patent No. 5464756
17	71	47.3	162	6	5464756-18 Patent No. 5464756
18	71	47.3	164	6	5464756-20 Patent No. 5464756
19	71	47.3	185	3	US-08-950-720A-12 Sequence 12, Appl
20	71	47.3	185	3	US-08-950-720A-13 Sequence 13, Appl
21	69	46.0	33	2	US-08-353-476-90 Sequence 90, Appl
22	68	45.3	29	2	US-08-483-476-1 Sequence 1, Appl
23	68	45.3	29	4	US-09-158-706-1 Patent No. 5464756
24	67	44.7	35	6	5464756-14 Patent No. 5464756
25	57	38.0	32	6	5464756-9 Patent No. 5464756
26	55	36.7	32	6	5464756-12 Patent No. 5464756
27	53	35.3	150	1	US-08-443-568B-12 Sequence 12, Appl

28 53 35.3 150 5 PCT-US94-06997-12 Sequence 12, Appl
29 53 35.3 188 2 US-08-905-267-2 Sequence 2, Appl
30 53 35.3 188 4 US-09-314-051-2 Sequence 2, Appl
31 51 34.0 35 6 5464756-13 Patent No. 5464756
32 49 32.7 213 2 US-08-905-267-13 Sequence 13, Appl
33 49 32.7 213 4 US-09-314-051-13 Sequence 23, Appl
34 48 32.0 603 4 US-09-097-889-23 Patent No. 5352575
35 47.5 31.7 577 6 5352575-9 Sequence 1, Appl
36 47 31.3 29 1 US-08-435-252-1 Patent No. 5470721
37 47 31.3 33 6 5470721-2 Patent No. 5489517
38 47 31.3 36 6 5489517-2 Patent No. 5489517
39 47 31.3 50 6 5436136-16 Patent No. 5436136
40 47 31.3 67 4 US-07-363-329A-2 Sequence 2, Appl
41 47 31.3 67 5 PCT-US92-09443A-2 Sequence 2, Appl
42 47 31.3 70 1 US-07-654-611-2 Sequence 2, Appl
43 47 31.3 70 1 US-08-180-572-5 Sequence 5, Appl
44 47 31.3 70 1 US-07-947-035-1 Sequence 1, Appl
45 47 31.3 70 1 US-07-776-272-17 Sequence 17, Appl

ALIGNMENTS

RESULT 1
5464756-16
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA: US/07/908,766
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:16:
; LENGTH: 30
5464756-16

Query Match 77.3%; Score 116; DB 6; Length 30;
Best Local Similarity 86.4%; Pred. No. 1.6e-10;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 GVRLCGREFIRAVITCGSRW 27
Db 9 GIRLCGREFIRAVITCGSRW 30
:::|||||:::|||||

RESULT 2
5464756-15
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:15:
; LENGTH: 29
5464756-15

Query Match 68.0%; Score 102; DB 6; Length 29;
Best Local Similarity 81.0%; Pred. No. 1.7e-08;
Matches 17; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 GVRLCGREFIRAVFTCGGSRW 26
 I:|||||I:|||||I:|||||I:|||||I:|||||
 Db 9 GIKLCGREFIRAVFTACGGSRW 29

RESULT 3
 US-08-353-476-92
 ; Sequence 92, Application US/08353476
 ; Patent No. 5871902

; GENERAL INFORMATION:
 ; APPLICANT: Weininger, Susan
 ; APPLICANT: Weininger, Arthur M
 ; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
 ; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
 ; NUMBER OF SEQUENCES: 117

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Saliwanchik & Saliwanchik
 ; STREET: 2421 N.W. 41st St., Suite A-1
 ; CITY: Gainesville
 ; STATE: Florida
 ; COUNTRY: USA
 ; ZIP: 32606

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/353,476
 ; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Beunen, Gerard H

; REGISTRATION NUMBER: 35,746

; REFERENCE/DOCKET NUMBER: GP-100

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (904) 375-8100

; TELEFAX: (904) 372-5800

; INFORMATION FOR SEQ ID NO: 92:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 40 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

US-08-353-476-92

Query Match 58.0%; Score 87; DB 2; Length 40;
 Best Local Similarity 70.0%; Pred. No. 3.6e-06;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVFTCGGSRW 27
 I:|||||I:|||||I:|||||I:|||||I:|||||
 Db 9 RLCGRDLIRAVFTLCGGTRW 28

RESULT 4
 US-08-950-720A-2
 ; Sequence 2, Application US/08950720A
 ; Patent No. 6046028

; GENERAL INFORMATION:

; APPLICANT: Conklin, Darrell C.

; APPLICANT: Lofton-Day, Catherine E.

; APPLICANT: Lok, Si

; APPLICANT: Jaspers, Stephen R.

; TITLE OF INVENTION: INSULIN HOMOLOG

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ZymoGenetics, Inc.

; STREET: 1201 Eastlake Avenue East
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/950,720A
 ; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Sawislak, Deborah A

; REGISTRATION NUMBER: 37,438

; REFERENCE/DOCKET NUMBER: 96-09

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-442-6672

; TELEFAX: 206-442-6678

; TELEX:

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 135 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

US-08-950-720A-2

Query Match 54.7%; Score 82; DB 3; Length 135;
 Best Local Similarity 66.7%; Pred. No. 6.5e-05;
 Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
 I:|||||I:|||||I:|||||I:|||||I:|||||
 Db 26 VRLCGLEYIRTVIICASSRW 46

RESULT 5

US-08-484-219-4

; Sequence 4, Application US/08484219

; Patent No. 5911997

; GENERAL INFORMATION:

; APPLICANT: Schwabe, Christian

; APPLICANT: Unemori, Elaine

; TITLE OF INVENTION: RELAXIN-LIKE FACTOR AND METHODS AND USES

; TITLE OF INVENTION: THEREOF

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/484,219

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Halluin, Albert P.

REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7842-040
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-219-4

Query Match 50.7%; Score 76; DB 2; Length 31;
Best Local Similarity 55.0%; Pred. No. 0.00011;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVFTCGSRW 27
:|||||:|||||
Db 8 KLCGHFVRALVRVCGPRW 27

RESULT 6
US-08-950-720A-14
; Sequence 14, Application US/08950720A
; Patent No. 6046028
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Lok, Si
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: INSULIN HOMOLOG
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,720A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046028e
US-08-950-720A-14

Query Match 50.7%; Score 76; DB 3; Length 101;
Best Local Similarity 55.0%; Pred. No. 0.00036;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVFTCGSRW 27
:|||||:|||||
Db 32 KLCGHFVRALVRVCGPRW 51

RESULT 7
US-08-950-720A-6
; Sequence 6, Application US/08950720A
; Patent No. 6046028
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Lok, Si
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: INSULIN HOMOLOG
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,720A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-950-720A-6

Query Match 50.0%; Score 75; DB 3; Length 135;
Best Local Similarity 52.4%; Pred. No. 0.00068;
Matches 11; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGSRW 27
:|||||:|||||
Db 26 VKLCGLDYVRTVIICASSRW 46

RESULT 8
US-08-443-568B-2
; Sequence 2, Application US/08443568B
; Patent No. 5759807
; GENERAL INFORMATION:
; APPLICANT: Breece, Tim

APPLICANT: Havenga, Kirk
APPLICANT: Rindersknecht, Ernst
APPLICANT: Vandlen, Richard
APPLICANT: Daniel, Yansura
TITLE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,568B
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/080,354
FILING DATE: 21-JUNE-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B.
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 7842-037
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-443-568B-2

Query Match 47.3%; Score 71; DB 1; Length 29;
Best Local Similarity 57.1%; Pred. NO. 0.00056;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Caps 0;

QY 7 VRLCGREFIRAVITCGGSRW 27
DB 8 IKLCGRELVRQAICGMSTW 28

RESULT 9
US-08-484-219-5
Sequence 5, Application US/08484219
Patent No. 5911997
GENERAL INFORMATION:
APPLICANT: Schwabe, Christian
APPLICANT: Unemori, Elaine
TITLE OF INVENTION: RELAXIN-LIKE FACTOR AND METHODS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,219
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7842-040
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-219-5

Query Match 47.3%; Score 71; DB 2; Length 29;
Best Local Similarity 57.1%; Pred. NO. 0.00056;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Caps 0;

QY 7 VRLCGREFIRAVITCGGSRW 27
DB 8 IKLCGRELVRQAICGMSTW 28

RESULT 10
PCT-US94-06997-2
Sequence 2, Application PC/TUS9406997
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: 460 Point San Bruno Boulevard
APPLICANT: South San Francisco, California
APPLICANT: United States of America
TITLE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06997
FILING DATE: 20-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7842-025-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown

; MOLECULE TYPE: protein
PCT-US94-06997-2

Query Match 47.3%; Score 71; DB 5; Length 29;
Best Local Similarity 57.1%; Pred. No. 0.00056;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGSRW 27
Db 8 IKLCGRELVAQIAICGMSTW 28

RESULT 11

5464756-11
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:11:
; LENGTH: 32
5464756-11

Query Match 47.3%; Score 71; DB 6; Length 32;
Best Local Similarity 57.1%; Pred. No. 0.00062;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGSRW 27
Db 7 IKLCGRELVAQIAICGMSTW 27

RESULT 12

5464756-10
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:10:
; LENGTH: 33
5464756-10

Query Match 47.3%; Score 71; DB 6; Length 33;
Best Local Similarity 57.1%; Pred. No. 0.00064;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGSRW 27
Db 8 IKLCGRELVAQIAICGMSTW 28

RESULT 13

US-08-443-568B-14
; Sequence 14, Application US/08443568B
; Patent No. 5759807

; GENERAL INFORMATION:
; APPLICANT: Breece, Tim
; APPLICANT: Hayenga, Kirk
; APPLICANT: Rindersknecht, Ernst
; APPLICANT: Vandlen, Richard
; APPLICANT: Daniel, Yansura
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,568B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/080,354
; FILING DATE: 21-JUNE-1993
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B.
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 7842-037

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-443-568B-14

Query Match 47.3%; Score 71; DB 1; Length 52;
Best Local Similarity 57.1%; Pred. No. 0.001;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGSRW 27
Db 31 IKLCGRELVAQIAICGMSTW 51

RESULT 14

PCT-US94-06997-14
; Sequence 14, Application PC/TUS9406997
; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.
; APPLICANT: 460 Point San Bruno Boulevard
; APPLICANT: South San Francisco, California
; APPLICANT: United States of America
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06997
; FILING DATE: 20-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7842-025-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-06997-14

Query Match 47.3%; Score 71; DB 5; Length 52;
Best Local Similarity 57.1%; Pred. No. 0.001;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVIFTCGSRW 27
DB 31 IKLCGRELVRQAIAICGMSTW 51

RESULT 15
US-08-443-568B-10
; Sequence 10, Application US/08443568B
; Patent No. 5759807
; GENERAL INFORMATION:
; APPLICANT: Breece, Tim
; APPLICANT: Hayenga, Kirk
; APPLICANT: Rindersknecht, Ernst
; APPLICANT: Vandien, Richard
; APPLICANT: Daniel, Yansura
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,568B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/080,354
; FILING DATE: 21-JUNE-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adams, Samuel B.
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 7842-037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-443-568B-10

Query Match 47.3%; Score 71; DB 1; Length 77;
Best Local Similarity 57.1%; Pred. No. 0.0015;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVIFTCGSRW 27
DB 19 IKLCGRELVRQAIAICGMSTW 39

Search completed: June 27, 2002, 16:08:44
Job time: 193 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2002, 16:09:27 ; Search time 36.01 Seconds
(without alignments)
72.047 Million cell updates/sec

Title: US-09-781-077-2_COPY_26_52

Perfect score: 150

Sequence: 1 RAAPYGVRLCGREFIRAVITCGGSRW 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	116	77.3	54	2	A26463		relaxin - spiny do
2	96	64.0	44	1	RXRROT		relaxin - sand tig
3	87	58.0	64	2	A29543		relaxin - little s
4	76	50.7	131	2	B53024		Leydig insulin-lik
5	75	50.0	131	2	A53024		Leydig insulin-lik
6	72	48.0	166	2	S42786		relaxin 2 precurs
7	71	47.3	57	2	S42784		relaxin - gorilla
8	71	47.3	166	2	S42783		relaxin 1 precurs
9	71	47.3	185	1	A44559		relaxin 1 precurs
10	71	47.3	185	1	A60982		relaxin 2 precurs
11	63	42.0	57	2	S42778		relaxin - gorilla
12	61	40.7	54	2	B32201		relaxin - minke wh
13	61	40.7	185	2	S48082		relaxin precursor
14	60	40.0	59	2	A53879		relaxin - dog (fra
15	57	38.0	33	2	I56451		relaxin - hamadrya
16	57	38.0	185	2	A34936		relaxin precursor
17	56	37.3	31	2	A58793		relaxin chain B -
18	55	36.7	54	2	A32201		relaxin - Bryde's
19	55	36.7	182	1	RXPQ		relaxin precursor
20	54	36.0	33	2	S42781		relaxin - oranguta
21	53	35.3	106	2	T27987		hypothetical prote
22	52	34.7	48	2	A49739		relaxin - horse (f
23	52	34.7	143	2	I47053		relaxin B,C and A
24	51	34.0	112	2	T29014		hypothetical prote
25	51	34.0	186	1	RXRT		relaxin precursor
26	51	34.0	886	2	A48586		suppressor of hair
27	50	33.3	24	2	S42785		relaxin - baboon (
28	50	33.3	187	2	T10897		insulin-like growt
29	50	33.3	448	2	S71427		transcription fact

30 50 33.3 449 2 S41647
31 49.5 33.0 106 2 T27989
32 49.5 33.0 235 2 T44466
33 49.5 33.0 372 2 T47344
34 49 32.7 52 1 INEN
35 49 32.7 59 1 INFI
36 49 32.7 59 1 INRO
37 49 32.7 107 2 T27988
38 48.5 32.3 375 2 F91115
39 48.5 32.3 375 2 F85960
40 48 32.0 140 2 G85746
41 48 32.0 140 2 D90872
42 48 32.0 140 2 AI0737
43 48 32.0 160 2 A49194
44 48 32.0 201 2 A48827
45 48 32.0 598 2 S55014

ALIGNMENTS

RESULT 1

A26463

relaxin - spiny dogfish (fragments)

C:Species: Squalus acanthias (spiny dogfish)

C:Date: 19-Nov-1988 #sequence_revision 26-May-1995 #text_change 26-May-1995

C:Accession: B26463; A26463

R:Bullesbach, E.E.; Gowan, L.K.; Schwabe, C.; Steinetz, B.G.; O'Byrne, E.; Callard, I.

Eur. J. Biochem. 161, 335-341, 1986

A:Title: Isolation, purification, and the sequence of relaxin from spiny dogfish (Squ

A:Reference number: A91179; MUID:87054035

A:Accession: B26463

A:Molecule type: protein

A:Residues: 'E',2-30 <BUL>

A:Experimental source: ovary

A>Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we h

A:Accession: A26463

A:Molecule type: protein

A:Residues: 31-54 <BU2>

A:Experimental source: ovary

C:Superfamily: insulin

C:Keywords: hormone; Pyroglutamic acid

F:1-30,31-54/Product: relaxin #status experimental <NAT>

F:1-30/Domain: chain B #status experimental <CHB>

F:31-54/Domain: chain A #status experimental <CHA>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:13-41,25-54,40-45/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 77.3%; Score 116; DB 2; Length 54;

Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 GVRLCGREFIRAVITCGGSRW 27

Db 9 GIKLCGREFIRAVITCGGSRW 30

RESULT 2

RXRROT

relaxin - sand tiger (tentative sequence) (fragments)

C:Species: Odontaspis taurus (sand tiger)

C:Date: 01-Sep-1981 #sequence_revision 26-May-1995 #text_change 31-Mar-2000

C:Accession: A01616

R:Gowan, L.K.; Reilig, J.W.; Schwabe, C.; Bedarkar, S.; Blundell, T.L.

FEBS Lett. 129, 80-82, 1981

A:Title: On the primary and tertiary structure of relaxin from the sand tiger shark (S

A:Reference number: A01616; MUID:82004703

A:Accession: A01616

A:Molecule type: protein

A:Residues: 1;2-19;21-44 <GOW>

R:Bullesbach, E.E.; Gowan, L.K.; Schwabe, C.; Steinetz, B.G.; O'Byrne, E.; Callard, I.

Eur. J. Biochem. 161, 335-341, 1986

A:Title: Isolation, purification, and the sequence of relaxin from spiny dogfish (Squalus elasmobranchus) cDNA.
 A:Reference number: A91179; MUID:87054035
 A:Contents: annotation; sequence revision
 A:Note: the carboxyl-terminal sequence of chain B was determined to be Arg-Trp
 C:Superfamily: Insulin
 C:Keywords: pyroglutamic acid
 F:1-19/Domain: chain B (fragments) #status experimental <CHB>
 F:21-44/Domain: chain A #status experimental <CHA>
 F:1/Modified site: Pyroglutamate carboxylic acid (Gln) #status experimental
 F:3-31,15-44,30-35/Disulfide bonds: #status predicted

Query Match 64.0%; Score 96; DB 1; Length 44;
 Best Local Similarity 80.0%; Pred. No. 1.9e-07;
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVIFTCGGSRW 27
 :|||||:|||||:|||||
 Db 1 QLCGRGIRAFIIFCGGSRW 20

RESULT 3
 A29543
 relaxin - little skate (fragments)
 C:Species: Raja erinacea (little skate)
 C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 16-Feb-1997
 C:Accession: A29543
 R:Bullesbach, E.E.; Schwabe, C.; Calliard, I.P.
 Biochem. Biophys. Res. Commun. 143, 273-280, 1987
 A:Title: Relaxin from an oviparous species, the skate (Raja erinacea).
 A:Reference number: A29543; MUID:87156758
 A:Accession: A29543
 A:Molecule type: protein
 A:Residues: 1-64 <BUL>
 A:Experimental source: ovary
 C:Superfamily: insulin

Query Match 58.0%; Score 87; DB 2; Length 64;
 Best Local Similarity 70.0%; Pred. No. 5.9e-06;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVIFTCGGSRW 27
 :|||||:|||||:|||||
 Db 9 RLCGRDLIRAFIYLCGGTRW 28

RESULT 4
 B53024
 Leydig insulin-like protein precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
 C:Accession: B53024; I54278
 R:Burkhardt, E.; Adham, I.M.; Brosig, B.; Gastmann, A.; Mattei, M.G.; Engel, W.
 Genomics 20, 13-19, 1994
 A:Title: Structural organization of the porcine and human genes coding for a Leydig cell
 A:Reference number: A53024; MUID:94292172
 A:Accession: B53024
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-131 <BUR>
 A:Cross-references: GB:X73637
 R:Burkhardt, E.; Adham, I.M.; Hobohm, U.; Murphy, D.; Sander, C.; Engel, W.
 Hum. Genet. 94, 91-94, 1994
 A:Title: A human cDNA coding for the Leydig insulin-like peptide (Ley I-L).
 A:Reference number: I54278; MUID:94307715
 A:Accession: I54278
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-131 <RES>
 A:Cross-references: GB:S72482; NID:G632798; PIDN:AA831371.1; PID:G632799
 C:Genetics:
 A:Gene: GDB:INSL3

A:Cross-references: GDB:230307; OMIM:146738
 A:Map position: 19p13.2-19p12
 A:Introns: 64/1

Query Match 50.7%; Score 76; DB 2; Length 131;
 Best Local Similarity 55.0%; Pred. No. 0.0005;
 Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVIFTCGGSRW 27
 :|||||:|||||:|||||
 Db 32 KLCGHHFVRALVRVCGGPRW 51

RESULT 5
 A53024
 Leydig insulin-like protein precursor - pig
 N:Alternate names: Ley I-L
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
 C:Accession: A53024; A49687
 R:Burkhardt, E.; Adham, I.M.; Brosig, B.; Gastmann, A.; Mattei, M.G.; Engel, W.
 Genomics 20, 13-19, 1994
 A:Title: Structural organization of the porcine and human genes coding for a Leydig cell
 A:Reference number: A53024; MUID:94292172
 A:Accession: A53024
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-131 <BUR>
 A:Cross-references: GB:X73636; NID:G871548; PIDN:CAA52016.1; PID:G871549
 R:Adham, I.M.; Burkhardt, E.; Benahmed, M.; Engel, W.
 J. Biol. Chem. 268, 26668-26672, 1993
 A:Title: Cloning of a cDNA for a novel insulin-like peptide of the testicular Leydig cell
 A:Reference number: A49687; MUID:94075362
 A:Accession: A49687
 A:Molecule type: mRNA
 A:Residues: 1-131 <ADH>
 A:Cross-references: GB:X58369
 A:Experimental source: testis
 A:Note: sequence extracted from NCBI backbone (NCBIN:140859, NCBIP:140860)
 C:Genetics:
 A:Gene: INSL3
 A:Map position: 19p13.2-pl2
 A:Introns: 64/1
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-56/Domain: Leydig insulin-like protein chain B #status predicted <BCH>
 F:57-105/Domain: connecting C peptide #status predicted <CPEP>
 F:106-131/Domain: Leydig insulin-like protein chain A #status predicted <ACH>

Query Match 50.0%; Score 75; DB 2; Length 131;
 Best Local Similarity 55.0%; Pred. No. 0.0007;
 Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVIFTCGGSRW 27
 :|||||:|||||:|||||
 Db 32 KLCGHHFVRALVRVCGGPRW 51

RESULT 6
 S42786
 relaxin 2 precursor - chimpanzee (fragment)
 C:Species: Pan troglodytes (chimpanzee)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
 C:Accession: S42786
 R:Evans, B.B.
 submitted to the EMBL Data Library, November 1993
 A:Reference number: S42776
 A:Accession: S42786
 A:Molecule type: mRNA
 A:Residues: 1-166 <EVA>
 A:Cross-references: EMBL:Z27245; NID:G416109; PIDN:CAA81758.1; PID:G416110
 C:Genetics:

A:Gene: rlx2
C:Superfamily: insulin
F:1-5/Domain: signal sequence (fragment) #status predicted <SIG>
F:6-166/Product: relaxin 2 #status predicted <MAT>

Query Match 48.0%; Score 72; DB 2; Length 166;
Best Local Similarity 57.1%; Pred. No. 0.0024; Mismatches 3; Indels 0; Gaps 0;

Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
:|||||:| | | | |
Db 13 IKLCGRELVRQAICGKSTW 33

RESULT 7
S42784
relaxin - gorilla (fragments)
C:Species: Gorilla gorilla (gorilla)
C:Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: S42784; S42779
R:Evans, B.B.
submitted to the EMBL Data Library, November 1993

A:Reference number: S42776
A:Accession: S42784
A:Molecule type: DNA
A:Residues: 1-33 <EVA>
A:CROSS-references: EMBL:Z27237; NID:G416010; PIDN:CAA81751.1; PID:G416011
A:Note: chain 2B
A:Accession: S42779
A:Molecule type: DNA
A:Residues: 34-57 <EVA>
A:CROSS-references: EMBL:Z27228; NID:G415952; PIDN:CAA81742.1; PID:G415953
A:Note: chain 2A
C:Genetics:
A:Gene: rlx2
C:Superfamily: insulin
C:Keywords: disulfide bond; hormone
F:1-33/Domain: relaxin chain 2B (fragment) #status predicted <RXB2>
F:34-57/Domain: relaxin chain 2A (fragment) #status predicted <RXA2>

Query Match 47.3%; Score 71; DB 2; Length 57;
Best Local Similarity 57.1%; Pred. No. 0.0013; Mismatches 3; Indels 0; Gaps 0;

Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
:|||||:| | | | |
Db 8 IKLCGRELVRQAICGKSTW 28

RESULT 8
S42783
relaxin 1 precursor - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C:Accession: S42783
R:Evans, B.B.

submitted to the EMBL Data Library, November 1993

A:Reference number: S42776
A:Accession: S42783
A:Molecule type: mRNA
A:Residues: 1-166 <EVA>
A:CROSS-references: EMBL:Z27225; NID:G415996; PIDN:CAA81739.1; PID:G415997
C:Genetics:
A:Gene: rlx1
C:Superfamily: insulin
C:Keywords: disulfide bond; hormone
F:1-5/Domain: signal sequence (fragment) #status predicted <SIG>
F:6-166/Product: relaxin 1 #status predicted <MAT>

Query Match 47.3%; Score 71; DB 2; Length 166;

Best Local Similarity 57.1%; Pred. No. 0.0035;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
:|||||:| | | | |
Db 13 IKLCGRELVRQAICGKSTW 33

RESULT 9
A44559
relaxin 1 precursor - human
N:Alternate names: preprorelaxin 1
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 07-Oct-1994 #text_change 18-Jun-1999
C:Accession: B05092; A44559
R:Hudson, P.; John, M.; Crawford, R.; Haralambidis, J.; Scanlon, D.; Gorman, J.; Tregear, E.M.B. J. 3, 2333-2339, 1984

A:Title: Relaxin gene expression in human ovaries and the predicted structure of a human relaxin.
A:Reference number: A05092; MUID:85051298
A:Accession: B05092
A:Molecule type: DNA
A:Residues: 1-185 <HU1>

A:CROSS-references: GB:X00949; NID:G35932; PIDN:CAA25461.1; PID:G35933
R:Hudson, P.; Haley, J.; John, M.; Cronk, M.; Crawford, R.; Haralambidis, J.; Tregear, E.M.B. J. 3, 2333-2339, 1984
A:Title: Structure of a genomic clone encoding biologically active human relaxin.
A:Reference number: A44559; MUID:83141755
A:Accession: A44559
A:Molecule type: DNA
A:Residues: 1-185 <HU2>

A:CROSS-references: GB:X00949; NID:G35932; PIDN:CAA25461.1; PID:G35933
C:Comment: Relaxin is an ovarian hormone that acts with estrogen to produce dilation of the cervix.
C:Genetics:
A:Gene: GDB:RLN1
A:CROSS-references: GDB:119552; OMIM:179730
A:Map position: 9pter-q12
C:Superfamily: insulin
C:Keywords: hormone; ovary

F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-57,162-185/Product: relaxin 1 chain B #status predicted <BCH>
F:58-138/Domain: relaxin 1 connecting C peptide #status predicted <MAT>
F:162-185/Domain: relaxin 1 chain A #status predicted <ACH>
F:35-172,47-185,171-176/Disulfide bonds: #status predicted

Query Match 47.3%; Score 71; DB 1; Length 185;
Best Local Similarity 57.1%; Pred. No. 0.0038; Mismatches 3; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
:|||||:| | | | |
Db 32 IKLCGRELVRQAICGKSTW 52

RESULT 10

A60982
relaxin 2 precursor [validated] - human

N:Alternate names: preprorelaxin 2
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 08-Dec-2000
C:Accession: A05092; A60982
R:Hudson, P.; John, M.; Crawford, R.; Haralambidis, J.; Scanlon, D.; Gorman, J.; Tregear, E.M.B. J. 3, 2333-2339, 1984

A:Title: Relaxin gene expression in human ovaries and the predicted structure of a human relaxin.
A:Reference number: A05092; MUID:85051298
A:Accession: A05092
A:Molecule type: mRNA
A:Residues: 1-185 <HUD>

A:CROSS-references: GB:X00948; NID:G35926; PIDN:CAA25460.1; PID:G35927
R:Stuts, J.F.; Bourell, J.H.; Canova-Davis, E.; Ling, V.T.; Laramee, G.R.; Winslow, B. J. 19, 655-664, 1990

A:Title: Structural characterization by mass spectrometry of native and recombinant human relaxin precursor - mouse
A:Reference number: A60982; MUID:91167739
A:Accession: B32201
A:Molecule type: protein
A:Residues: 25-53;162-185 <STU>
C:Genetics:
A:Gene: GDB:RLN2
A:Cross-references: GDB:119553; QMIM:179740
A:Map position: 9pter-9q12
C:Superfamily: insulin
C:Keywords: ovary; pyroglutamic acid
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-53/Domain: relaxin 2 chain B #status experimental <BCH>
F:53-162/Domain: relaxin 2 #status experimental <MAT>
F:58-157/Domain: relaxin 2 connecting C peptide #status predicted <CPEP>
F:162-185/Domain: relaxin 2 chain A #status experimental <ACH>
F:35-172,47-185,171-176/Disulfide bonds: #status experimental
F:162/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental

Query Match 47.3%; Score 71; DB 1; Length 185;
Best Local Similarity 57.1%; Pred. No. 0.0038;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVIFTCGSRW 27
:::|||||:::|||||
Db 32 IKLCGELVRAQIAICGMSTW 52

RESULT 11
S42778
relaxin - gorilla (fragments)
C:Species: Gorilla gorilla (gorilla)
C:Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: S42778; S42777
R:Evans, B.B.
submitted to the EMBL Data Library, November 1993
A:Reference number: S42776
A:Accession: S42778
A:Molecule type: DNA
A:Residues: 1-33 <EVA>
A:Cross-references: EMBL:Z27227; NID:g415950; PIDN:CAA81741.1; PID:g415951
A:Note: chain 1B
A:Accession: S42777
A:Molecule type: DNA
A:Residues: 34-57 <EVX>
A:Cross-references: EMBL:Z27226; NID:g415948; PIDN:CAA81740.1; PID:g415949
A:Note: chain 1A
C:Genetics:
A:Gene: rlx1
C:Superfamily: insulin
C:Keywords: disulfide bond; hormone
F:1-33/Domain: relaxin chain 1B (fragment) #status predicted <RXBL>
F:34-57/Domain: relaxin chain 1A (fragment) #status predicted <RXAL>

Query Match 42.0%; Score 63; DB 2; Length 57;
Best Local Similarity 52.4%; Pred. No. 0.021;
Matches 11; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVIFTCGSRW 27
:::|||||:::|||||
Db 8 IKLCGELVRAQIAICGMSTW 28

RESULT 12
B32201
relaxin - minke whale (fragments)
C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Jun-1993
C:Accession: B32201
R:Schwabe, C.; Buellesbach, E.E.; Heyn, H.; Yoshioka, M.
J. Biol. Chem. 264, 940-943, 1989

A:Title: Cetacean relaxin. Isolation and sequence of relaxins from Balaenoptera acuto
A:Reference number: A32201; MUID:89093167
A:Accession: B32201
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-54 <SCH>
C:Superfamily: insulin

Query Match 40.7%; Score 61; DB 2; Length 54;
Best Local Similarity 42.9%; Pred. No. 0.039;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVIFTCGSRW 27
:::|||||:::|||||
Db 7 IKACGRELVLWVEICGSVRW 27

RESULT 13
S48082
relaxin precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 16-Jul-1999
C:Accession: S48082; PC2067; PN0626
R:Evans, B.A.; John, M.; Fowler, K.J.; Summers, R.J.; Cronk, M.; Shine, J.; Tregear, J. Mol. Endocrinol. 10, 15-23, 1993
A:Title: The mouse relaxin gene: nucleotide sequence and expression.
A:Reference number: S48082; MUID:93199663
A:Accession: S48082
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-185 <EVA>
A:Cross-references: EMBL:Z27088; NID:g414780; PIDN:CAA81611.1; PID:g414781
R:Buellesbach, E.E.; Schwabe, C.
Biochem. Biophys. Res. Commun. 196, 311-319, 1993
A:Title: Mouse relaxin: synthesis and biological activity of the first relaxin with a
A:Reference number: PN0626; MUID:94030011
A:Accession: PC2067
A:Molecule type: protein
A:Residues: 23-57 <BUE>
A:Accession: PN0626
A:Molecule type: protein
A:Residues: 161-185 <BU2>
A:Note: proteins with and without 184-Tyr were synthesized, their biological activity
C:Superfamily: insulin
C:Keywords: hormone
F:23-57,161-185/Product: relaxin #status experimental <MAT>
F:23-57/Domain: chain B #status experimental <CHB>
F:161-185/Domain: chain A #status experimental <CHA>
F:36-171,48-185,170-175/Disulfide bonds: #status experimental

Query Match 40.7%; Score 61; DB 2; Length 185;
Best Local Similarity 52.6%; Pred. No. 0.12;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVIFTCGGS 25
:::|||||:::|||||
Db 33 IRMCGREYARELIKCGAS 51

RESULT 14
A53879
relaxin - dog (fragments)
C:Species: Canis lupus familiaris (dog)
C:Date: 27-Sep-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C:Accession: B53879; A53879
R:Stewart, D.R.; Henzel, W.J.; Vandlen, R.
J. Protein Chem. 11, 247-253, 1992
A:Title: Purification and sequence determination of canine relaxin.
A:Reference number: A53879; MUID:93000391
A:Accession: B53879
A:Molecule type: protein

A;Residues: 1-35 <STE>
 A;Experimental source: placenta
 A;Note: sequence extracted from NCBI backbone (NCBIP:115401)
 A;Accession: A53879
 A;Molecule type: protein
 A;Residues: 36-59 <ST2>
 A;Experimental source: placenta
 A;Note: sequence extracted from NCBI backbone (NCBIP:115399)
 C;Superfamily: insulin
 C;Keywords: hormone
 F;1-35/36-59/Product: relaxin #status experimental <MAT>
 F;1-35/Domain: chain B #status experimental <CHB>
 F;36-59/Domain: chain A #status experimental <CHA>
 F;9-46,21-59,45-50/Disulfide bonds: #status predicted

Query Match 40.0%; Score 60; DB 2; Length 59;
 Best Local Similarity 42.9%; Pred. No. 0.06;
 Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVIFTCGGRW 27
 :: |||:::| | || |
 Db 6 LKACGRDVRQLQIEVCGSSW 26

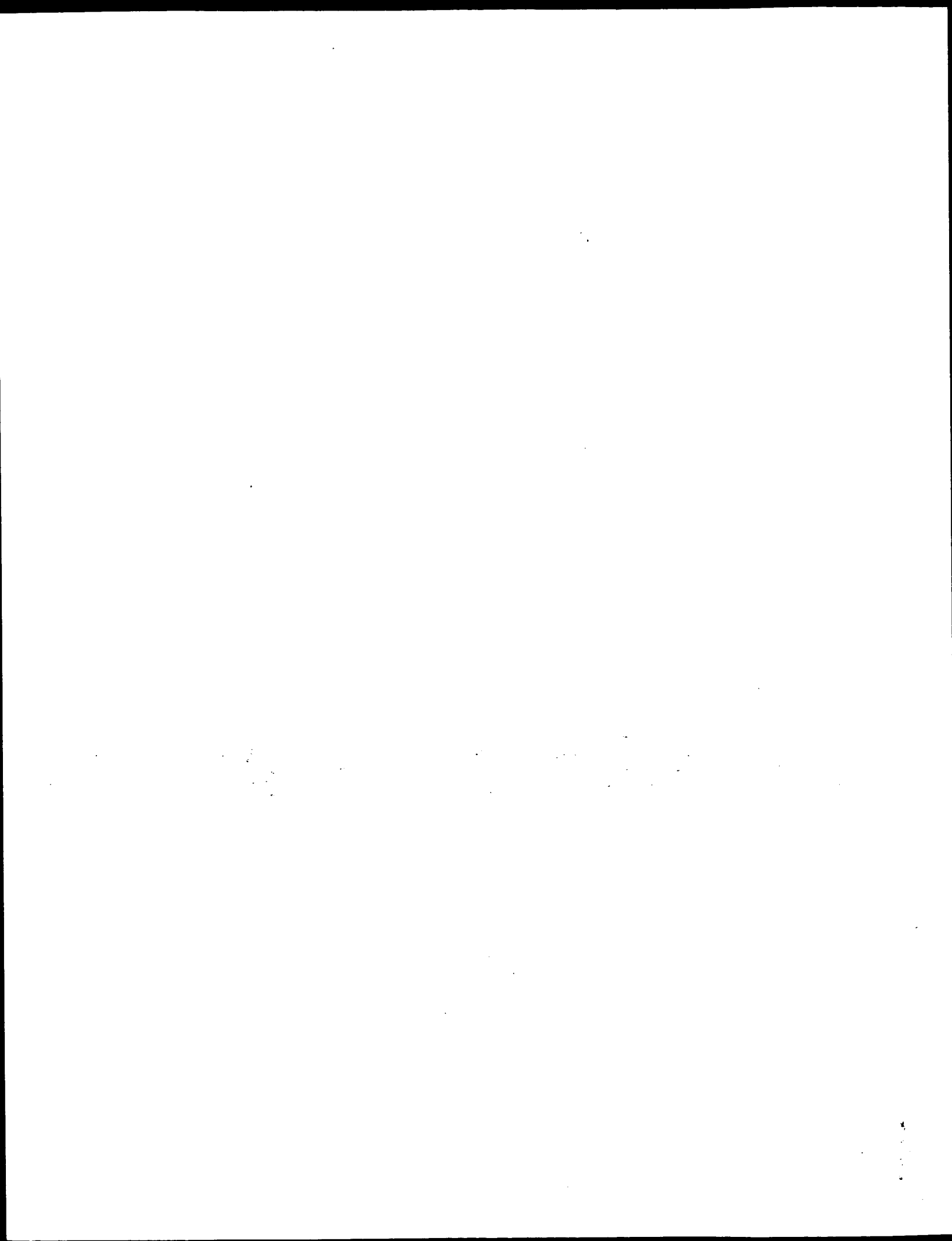
RESULT 15

I56451
 relaxin - hamadryas baboon (fragment)
 C;Species: Papio hamadryas (hamadryas baboon)
 C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 01-Dec-2000
 C;Accession: I56451; S42782
 J. Evans, B.B.A.; Fu, P.; Tregear, G.G.W.
 J. Mol. Endocrinol. 140, 385-392, 1994
 A;Title: Characterization of two relaxin genes in the chimpanzee.
 A;Reference number: I56451
 A;Accession: I56451
 A;Status: Preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-33 <EVA>
 A;Cross-references: EMBL:Z27224; NID:g415994; PIDN:CAAB1738.1; PID:g415995
 A;Note: submitted to the EMBL Data Library, November 1993
 C;Genetics:
 A;Gene: rlx
 C;Superfamily: insulin
 C;Keywords: hormone
 F;1-33/Domain: relaxin chain B (fragment) #status predicted <RXB>

Query Match 38.0%; Score 57; DB 2; Length 33;
 Best Local Similarity 52.6%; Pred. No. 0.1;
 Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVIFTCGGS 25
 :: |||| :|| | || |
 Db 8 IKACGRELVRQIAICGKS 26

Search completed: June 27, 2002, 16:09:27
 Job time: 211 sec




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RA Bullesbach E.E., Schwabe C., Callard I.P.:
RL "Relaxin from an oviparous species, the skate (Raja erinacea).";
RL Biochem. Biophys. Res. Commun. 143:273-280(1987).
CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS.
CC
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC
DR PIR: A29543; A29543.
DR HSP; P04090; 6RLX.
DR InterPro: IPR000739; Insulin_IGF_relaxin.
DR Pfam: PF00049; Insulin; 1.
DR SMART: SM00078; IIGF; 1.
DR PROSITE: PS00262; INSULIN; 1.
DR Insulin family; Hormone.
CC
CC CHAIN 1 40 RELAXIN B CHAIN.
CC NON_CONS 40 41
CC CHAIN 41 64 RELAXIN A CHAIN.
CC DISULFID 11 51 INTERCHAIN.
CC DISULFID 23 64 INTERCHAIN.
CC DISULFID 50 55
CC SEQUENCE 64 AA; 7499 MW; E7AC62B8BA81F49D CRC64;

Query Match 58.0%; Score 87; DB 1; Length 64;
Best Local Similarity 70.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0.

QY 8 RLCGRFETRAVFTCGGSRW 27
|||||: ||| |: |||: ||
DB 9 RLCGRDLRAFIYLCGGTRW 28

RESULT 4
INL5 HUMAN STANDARD; PRT; 135 AA.
AC QY5Q6;
AD 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Insulin-like peptide INSL5 precursor (Insulin-like peptide 5).
DE INSL5.
GN Homo sapiens (Human),
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX TISSUE=Colon;
RX MEDLINE=99389725; PubMed=10458910;
RA Conklin D., Lofton-Day C.E., Haldeman B.A., Ching A., Whitmore T.E.,
RA Lok S., Jaspers S.;
RA "Identification of INSL5, a new member of the insulin superfamily.";
RL Genomics 60:50-56(1999).
CC -!- FUNCTION: MAY HAVE A ROLE IN GUT CONTRACTILITY OR IN THYMIC
CC DEVELOPMENT AND REGULATION.
CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN RECTUM WITH LOWER LEVELS
CC IN UTERUS AND ASCENDING AND DESCENDING COLON.
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF133816; AAD29686.1; -
CC MIM: 606413;
DR InterPro: IPR000739; Insulin_IGF_relaxin.
DR SMART; SM00078; IIGF; 1.

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DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 48 INSULIN-LIKE PEPTIDE INSL5 B CHAIN
FT CHAIN 19 48 (POTENTIAL).
FT PROPEP 49 114 CONNECTING PEPTIDE (POTENTIAL).
FT CHAIN 115 135 INSULIN-LIKE PEPTIDE INSL5 A CHAIN
FT CHAIN 115 135 (POTENTIAL).
FT DISULFID 29 122 INTERCHAIN (BY SIMILARITY).
FT DISULFID 41 135 INTERCHAIN (BY SIMILARITY).
FT DISULFID 121 126 BY SIMILARITY.
SQ SEQUENCE 135 AA; 15318 MW; 98FFCB20E9C4BC1F CRC64;

Query Match 54.7%; Score 82; DB 1; Length 135;
Best Local Similarity 66.7%; Pred No. 1.9e-05;
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFTRAVITFCGSRW 27
Db 26 VRLCGLEYIRTVIYCASSRW 46
||||| I::I I::I I::I

RESULT 5
INL3_HUMAN STANDARD; PRT; 131 AA.
AC P51460; Q9UEA2;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
GN INSL3 OR RLF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Burkhardt E., Adham I.M., Hobohm U., Murphy D., Sander C., Engel W.;
RT "A human cDNA coding for the Leydig insulin-like peptide (Ley I-L).";
RL Hum. Genet. 94:91-94(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292172; PubMed=8020942;
RA Burkhardt E., Adham I.M., Brosig B., Gastmann A., Mattei M.-G.,
RA Engel W.;
RT "Structural organization of the porcine and human genes coding for a
RT Leydig cell-specific insulin-like peptide (LEY I-L) and chromosomal
RT localization of the human gene (INSL3).";
RL Genomics 20:13-19(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Vliswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Attix C., Andreise T., Frankheim M., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
RA Arellano A., Saunders C., Ow D., Nolan P., Trong S., Kobayashi A.,
RA Olsen A.S., Carraro A.V.;
RT "Sequence analysis of an ~700 kb region in 19p13.1 between JAK3 and
RT PDE4C."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
CC -!- SPERMATOGENESIS.
CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC -!- DISULFIDE BONDS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN PRENATAL AND
CC POSTNATAL LEYDIG CELLS. FOUND AS WELL IN THE CORPUS LUTEUM,
CC TROPHOBLAST, FETAL MEMBRANES AND BREAST.

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CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S72482; AAB31371.1; .
DR EMBL; X73637; CAA52017.1; ALT_SEQ.
DR EMBL; AC005952; AAC72277.1; .
DR MIM; 146738; .
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR Pfam; PF00049; Insulin; 1.
DR SMART; SM00078; ILGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 55 LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
FT PROPEP 58 104 C PEPTIDE (POTENTIAL).
FT CHAIN 106 131 LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
FT DISULFID 34 116 INTERCHAIN (BY SIMILARITY).
FT DISULFID 46 129 INTERCHAIN (BY SIMILARITY).
FT DISULFID 115 120 BY SIMILARITY.
FT CONFLICT 60 60 A -> T (IN REF. 3).
SQ SEQUENCE 131 AA; 14472 MW; C5799D610424C136 CRC64;

Query Match 50.7%; Score 76; DB 1; Length 131;
Best Local Similarity 55.0%; Pred. No. 0.00015;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLCGREFTRAVITFCGSRW 27
Db 32 KLCGHFVRLVRCVGGPRW 51
||||| I::I I::I I::I

RESULT 6
INL3_PIG STANDARD; PRT; 131 AA.
AC P51461;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
GN INSL3 OR RLF.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=94075362; PubMed=8253799;
RA Adham I.M., Burkhardt E., Benahmed M., Engel W.;
RT "Cloning of a cDNA for a novel insulin-like peptide of the testicular
RT Leydig cells."
RL J. Biol. Chem. 268:26668-26672(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292172; PubMed=8020942;
RA Burkhardt E., Adham I.M., Brosig B., Gastmann A., Mattei M.-G.,
RA Engel W.;
RT "Structural organization of the porcine and human genes coding for a
RT Leydig cell-specific insulin-like peptide (LEY I-L) and chromosomal
RT localization of the human gene (INSL3).";
RL Genomics 20:13-19(1994).
CC -!- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
CC SPERMATOGENESIS.
CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS (BY SIMILARITY).

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--!- SUBCELLULAR LOCATION: Secreted.
--!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN PRENATAL AND POSTNATAL LEYDIG CELLS.
--!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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-----
EMBL; X73636; CAAS2016.1; -.
DR EMBL; X68369; CAA48449.1; -.
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR Pfam; PF00049; Insulin; 1.
DR SMART; SM00078; IGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Signal.
FT SIGNAL          1      24    POTENTIAL.
FT CHAIN           25     56    LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
FT PROPEP         58    103    C PEPTIDE (POTENTIAL).
FT CHAIN          106    131    LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
FT DISULFD        34    116    INTERCHAIN (BY SIMILARITY).
FT DISULFD        46    129    INTERCHAIN (BY SIMILARITY).
FT DISULFD       115    120    BY SIMILARITY.
FT SEQUENCE       131 AA; 14134 MW; 8AB71B870859EF3A CRC64;
Query Match              50.0%; Score 75; DB 1; Length 131;
Best Local Similarity   55.0%; Pred. No. 0.00021;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY      8 RLCGRFFTRAVIFTCGGSRW 27
      :||| |:::||: ||| ||
Db     32 KLCGHHFYRLVRLCGGPRW 51
-----
RESULT 7
INL3_BOVIN
AC      INL3_BOVIN STANDARD; PRT; 132 AA.
ID      077801;
DT      16-OCT-2001 (Rel. 40, Created)
DD      16-OCT-2001 (Rel. 40, Last sequence update)
DE      16-OCT-2001 (Rel. 40, Last annotation update)
DN      Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
GN      INSL3 OR RLF.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxId=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RS      TISSUE=Testis;
RX      MEDLINE=97107158; PubMed=8949906;
RA      Rathgave R.A.D., Balvers M., Hunt N., Ivell R.;
RT      "Relaxin-like factor gene is highly expressed in the bovine ovary of the cycle and pregnancy: sequence and messenger ribonucleic acid analysis."
RT      Biol. Reprod. 55:1452-1457(1996).
RL      FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND SPERMATOGENESIS.
CC      SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS (BY SIMILARITY).
--!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN LEYDIG CELLS.
--!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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CC - I - SUBCELLULAR LOCATION: Secreted.

PROMOTING GROWTH OF PUBIC LIGAMENTS AND RIPENING OF THE CERVIX.

CC DISULFIDE BONDS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE CORPUS LUTEUM OF PREGNANCY
CC BUT NOT IN THE PLACENTA.
CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC -----
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CC -----
DR EMBL; 227225; CAA81739.1; -
DR HSP; P04090; 6RLX.
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR Pfam; PF00049; Insulin; 1.
DR SMART; SM00078; IIGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Multigene family; Signal.
FT NON_TER 1 1
FT SIGNAL <1 5
FT CHAIN 6 34 RELAXIN B CHAIN (PROBABLE).
FT PROPEP 37 139 CONNECTING PEPTIDE (PROBABLE).
FT CHAIN 143 166 RELAXIN A CHAIN (PROBABLE).
FT DISULFID 16 153 INTERCHAIN (BY SIMILARITY).
FT DISULFID 28 166 INTERCHAIN (BY SIMILARITY).
FT DISULFID 152 157 BY SIMILARITY.
SO SEQUENCE 166 AA; 18730 MW; 7F469B1F9259F4F CRC64;

Query Match 47.3%; Score 71; DB 1; Length 166;
Best Local Similarity 57.1%; Pred. No. 0.0011;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Oy 7 VRLCGREFIRAVIFTCGSRW 27
Db 13 IKLCGRELVRQIAICGMSTW 33

RESULT 11
ID REL1_HUMAN STANDARD; PRT; 185 AA.
AC P04808; O99936;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Prorelaxin H1 precursor.
GN RLN1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=85051296; PubMed=6548702;
RA Hudson P., John M., Crawford R., Haralambidis J., Scanlon D.,
RA Gorman J., Tregear G., Shine J., Niall H.;
RT "Relaxin gene expression in human ovaries and the predicted structure
RT of a human prorelaxin by analysis of cDNA clones.";
RL EMBO J. 3:2333-2339(1984).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=83141755; PubMed=6298628;
RA Hudson P., Haley J., John M., Cronk M., Crawford R., Haralambidis J.,
RA Tregear G., Shine J., Niall H.;
RT "Structure of a genomic clone encoding biologically active human
RT relaxin.";
RL Nature 301:628-631(1983).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Sehra H.;

Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE-Prostate;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
[5]
RN PARTIAL SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
RP SPECIFICITY.
RC TISSUE-Prostate;
RX MEDLINE=96328899; PubMed=8735594;
RA Gunnarsen J.W., Fu P., Roche P.J., Tregear G.W.;
RT "Expression of human relaxin genes: Characterization of a novel
RT alternatively-spliced human relaxin mRNA species.";
RL Mol. Cell. Endocrinol. 118:85-94(1996).
CC -1- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO
CC PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS. MAY BE
CC INVOLVED IN REMODELING OF CONNECTIVE TISSUES DURING PREGNANCY.
CC PROMOTING GROWTH OF PUBIC LIGAMENTS AND RIPENING OF THE CERVIX.
CC -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Prostate. Not expressed in placenta, decidua
CC or ovary.
CC -1- MISCELLANEOUS: H1 RELAXIN MAY BE A PSEUDOGENE.
CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC -----
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CC -----
DR EMBL; X00949; CAA25461.1; -
DR EMBL; V00578; CAA23839.1; -
DR EMBL; V00577; CAA23838.1; -
DR EMBL; A06926; CAA00603.1; -
DR EMBL; A06846; CAA00599.1; -
DR EMBL; A07364; CAA00658.1; -
DR EMBL; A07329; CAA01325.1; -
DR EMBL; A1135786; CAC04179.1; -
DR EMBL; BC005956; AAH05956.1; -
DR EMBL; S83200; AAD14429.1; -
DR PIR; A44559; A44559.
DR HSP; P04090; 6RLX.
DR MIM; 179730; -
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR Pfam; PF00049; Insulin; 1.
DR PRINTS; PR00276; INSULINA.
DR SMART; SM00078; IIGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Multigene family; Signal;
KW Alternative splicing; Polymorphism.
FT SIGNAL 1 22 PROBABLE.
FT CHAIN 23 53 RELAXIN B CHAIN (PROBABLE).
FT PROPEP 56 158 CONNECTING PEPTIDE (PROBABLE).
FT CHAIN 163 185 RELAXIN A CHAIN (PROBABLE).
FT DISULFID 35 172 INTERCHAIN (BY SIMILARITY).
FT DISULFID 47 185 INTERCHAIN (BY SIMILARITY).
FT DISULFID 171 176 BY SIMILARITY.
FT VARSPLIC 71 117 EIVPSFINKDTETIIIMLEFANLPPELKAALSERQPSLPE
FT LOQYVP -> GDFIOTVIGISPDGKALRTGSCFTREFLG
FT ALSKLYHPSSTKIOKL (IN ISOFORM 2).
FT MISSING (IN ISOFORM 2).
FT K -> M (IN DBSNP:618066).
FT /FTIG-VAR_011962.
FT SEQUENCE 185 AA; 21145 MW; B318628ABFEC7142 CRC64;

Query Match 47.3%; Score 71; DB 1; Length 185;
 Best Local Similarity 57.1%; Pred. No. 0.0012; 6; Indels 0; Gaps 0;
 Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
 Db 32 IKLCGRELVRQAICGMSTW 52

RESULT 12
 REL2_HUMAN STANDARD; PRT; 185 AA.
 AC P04090; Q9UCX3; Q99936;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Prorelaxin H2 precursor.
 GN RLN2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
 RX MEDLINE=85051298; PubMed=6548702;
 RA Hudson P., John M., Crawford R., Haralambidis J., Scanlon D.,
 RA Gorman J., Tregear G., Shine J., Niall H.;
 RT "Relaxin gene expression in human ovaries and the predicted structure
 of a human prorelaxin by analysis of cDNA clones.";
 RL EMBO J. 3:2333-2339(1984).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RA Sehra H.;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP PARTIAL SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
 RP SPECIFICITY.
 RC TISSUE=Prostate;
 RX MEDLINE=96328899; PubMed=8735594;
 RA Gunnerson J.M., Fu P., Roche P.J., Tregear G.W.;
 RT "Expression of human relaxin genes: characterization of a novel
 alternatively-spliced human relaxin mRNA species.";
 RL Mol. Cell. Endocrinol. 118:85-94(1996).
 RN [4]
 RP SYNTHESIS.
 RX MEDLINE=91250367; PubMed=2040595;
 RA Buellbach E.E., Schwabe C.;
 RT "Total synthesis of human relaxin and human relaxin derivatives by
 solid-phase peptide synthesis and site-directed chain combination.";
 RL J. Biol. Chem. 266:10734-10761(1991).
 RN [5]
 RP PARTIAL SEQUENCE OF 25-51.
 RC TISSUE=Semen;
 RX MEDLINE=92241162; PubMed=1572287;
 RA Winslow J.W., Shih A., Bourell J.H., Weiss G., Reed B., Stults J.T.,
 RA Goldsmith L.T.,
 RT "Human seminal relaxin is a product of the same gene as human luteal
 relaxin.";
 RL Endocrinology 130:2660-2668(1992).
 RN [6]
 RP SEQUENCE OF 25-53 AND 162-185.
 RX MEDLINE=91167739; PubMed=2076464;
 RA Winslow J.W., Griffin P.R., Rinderknecht E., Vandlen R.L.;
 RT "Structural characterization by mass spectrometry of native and
 recombinant human relaxin.";
 RL Biomed. Environ. Mass Spectrom. 19:655-664(1990).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RX MEDLINE=92015205; PubMed=1656049;
 RA Eigenbrot C., Randal M., Quan C., Burnier J., O'Connell L.,
 RA Rinderknecht E., Kossiakoff A.A.;
 RT "X-ray structure of human relaxin at 1.5 A. Comparison to insulin and
 implications for receptor binding determinants.";

J. Mol. Biol. 221:15-21(1991).
 -!- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO
 PRODUCE DILATION OF THE BIRTH CANAL IN MANY MAMMALS. MAY BE
 INVOLVED IN REMODELING OF CONNECTIVE TISSUES DURING PREGNANCY.
 PROMOTING GROWTH OF PUBIC LIGAMENTS AND RIPENING OF THE CERVIX.
 -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
 DISULFIDE BONDS.
 -!- SUBCELLULAR LOCATION: Secreted.
 -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 produced by alternative splicing.
 -!- TISSUE SPECIFICITY: Expressed in the ovary during pregnancy. Also
 expressed in placenta, decidua and prostate.
 -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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 EMBL; X00948; CAA25460.1; -;
 EMBL; AL135786; CAC04177.1; -;
 EMBL; AL135786; CAC04176.1; -;
 EMBL; S83200; AAD14429.1; -;
 EMBL; A17315; CAA01324.1; -;
 EMBL; A05925; CAA00602.1; -;
 PIR; A60982; A60982.
 PDB; 6RLX; 31-OCT-93.
 MIM; 179740; -;
 InterPro: IPR000739; Insulin_IGF_relaxin.
 Pfam; PF00049; Insulin; 1.
 SMART; SM00078; IIGF; 1.
 PROSITE; PS00262; INSULIN; 1.
 Insulin family; Hormone; Multigene family; Signal; 3D-structure;
 Alternative splicing.
 FT SIGNAL 1 24
 FT CHAIN 25 53 RELAXIN B CHAIN.
 FT PROPEP 56 157 CONNECTING PEPTIDE.
 FT CHAIN 162 185 RELAXIN A CHAIN.
 FT MOD_RES 162 162 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 35 172 INTERCHAIN.
 FT DISULFID 47 185 INTERCHAIN.
 FT DISULFID 171 176
 FT VARSPLIC 71 117
 FT
 FT
 FT VARSPLIC 118 185
 FT HELIX 27 29
 FT STRAND 31 32
 FT HELIX 36 49
 FT HELIX 163 173
 FT TURN 174 174
 FT STRAND 176 177
 FT HELIX 178 182
 FT TURN 183 184
 SQ SEQUENCE 185 AA; 21042 MW; AC73DBDE2090091B CRC64;
 Query Match 47.3%; Score 71; DB 1; Length 185;
 Best Local Similarity 57.1%; Pred. No. 0.0012;
 Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
 Db 32 IKLCGRELVRQAICGMSTW 52

RESULT 13
 INL3_RAT
 ID INL3_RAT
 AC Q9WUK0;

```

DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leydig insulin-like peptide (Ley-I-L) (Relaxin-like factor)
DE (fragment).
DE INSL3 OR RLF.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=SPRAGUE-DAWLEY;
RC Spleen A.-N., Pusch W., Ivell R.;
RA "Cloning and sequence of the rat relaxin-like factor and its
RT promoter";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
CC SPERMATOGENESIS.
CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT/TRUNCATED FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN THE LEYDIG CELLS OF THE
CC TESTIS.
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC
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CC
CC EMBL; AF139918; AAD33663.1;
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR Pfam; PF00049; Insulin; 1.
DR SMART; SM00078; ILGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone.
FT NON_TER 1
FT CHAIN <1 ? LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
FT PROPEP 77 C PEPTIDE (POTENTIAL).
FT CHAIN 80 105 LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
FT DISULFID 6 90 INTERCHAIN (BY SIMILARITY).
FT DISULFID 18 103 INTERCHAIN (BY SIMILARITY).
FT DISULFID 89 94 BY SIMILARITY.
FT SEQUENCE 105 AA; 11674 MW; 903716A8FBEB13EE CRC64;
SQ
Query Match 46.7%; Score 70; DB 1; Length 105;
Best Local Similarity 50.0%; Pred. No. 0.00096;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 8 RLCGREFIRAVITCGSRW 27
DB 4 KLCGHHVLRVVRVCGGPRW 23
RESULT 14
INL3 CALJA
ID INL3_CALJA STANDARD; PRT; 131 AA.
AC O97937; O97938;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
DE INSL3 OR RLF.
GN Callithrix jacchus (Common marmoset).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99115234; PubMed=9916013;
RA Zarreh-Hoshyari-Khah M., Einspanier A., Ivell R.;
RT "Differential splicing and expression of the relaxin-like factor gene
in reproductive tissues of the marmoset monkey (Callithrix jacchus).";
RL Biol. Reprod. 60:445-453(1999).
CC -!- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
CC SPERMATOGENESIS.
CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT/TRUNCATED FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN THE LEYDIG CELLS OF THE
CC TESTIS.
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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CC
CC EMBL; AJ011961; CAA09888.1;
DR EMBL; AJ011962; CAA09888.1; JOINED.
DR EMBL; AJ011961; CAA09889.1;
DR HSP; P01315; 1ZEI.
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR Pfam; PF00049; Insulin; 1.
DR SMART; SM00078; ILGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Signal; Alternative splicing.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 55 LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
FT PROPEP 58 104 C PEPTIDE (POTENTIAL).
FT CHAIN 107 131 LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
FT DISULFID 34 117 INTERCHAIN (BY SIMILARITY).
FT DISULFID 46 130 INTERCHAIN (BY SIMILARITY).
FT DISULFID 116 121 BY SIMILARITY.
FT VARSPLIC 64 74 GELLOWLERH -> ESHSAAQDGGQ (IN SHORT
FT ISOFORM).
FT VARSPLIC 75 131 MISSING (IN SHORT ISOFORM).
FT SEQUENCE 131 AA; 14252 MW; 685743CAEECF8731 CRC64;
SQ
Query Match 46.0%; Score 69; DB 1; Length 131;
Best Local Similarity 50.0%; Pred. No. 0.0017;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 8 RLCGREFIRAVITCGSRW 27
DB 32 KLCGHHVLRVVRVCGGPLW 51
RESULT 15
INL3 MOUSE
ID INL3_MOUSE STANDARD; PRT; 122 AA.
AC O09107; P97744;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
DE INSL3 OR RLF.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Zimmermann S.H.;

```

Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

[2]

SEQUENCE FROM N.A.
TISSUE=Testis;
MEDLINE=96366811; PubMed=8770925;
Rusch W., Balvers M., Ivell R.;
"Molecular cloning and expression of the relaxin-like factor from the
mouse testis";
Endocrinology 137:3009-3013(1996).
[3]

SEQUENCE FROM N.A.
STRAIN=129/SVJ;
MEDLINE=98088907; PubMed=9428631;
Koskimies P., Spiess A.N., Lahti P., Huhtaniemi I., Ivell R.;
"The mouse relaxin-like factor gene and its promoter are located
within the 3' region of the JAK3 genomic sequence.";
FEBS Lett. 419:186-190(1997).

-1- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
SPERMATOGENESIS.
-1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
DISULFIDE BONDS (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN LEYDIG CELLS.
-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

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EMBL; X95603; CAA64861.1; -
EMBL; S82815; AAB39365.1; -
EMBL; AF136524; AAD24585.1; -
MGD; MGI:108427; Insl3.
InterPro: IPR000739; Insulin_IGF_relaxin.
Pfam: PF00049; Insulin; 1.
SMART; SM00078; ILGF; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Signal.
SIGNA 1 15
CHAIN 16 ?
FT POTENTIAL.
FT LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
FT C PEPTIDE (POTENTIAL).
FT LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
FT INTERCHAIN (BY SIMILARITY).
FT INTERCHAIN (BY SIMILARITY).
FT BY SIMILARITY.
FT P -> T (IN REF. 1).
FT VETRD -> CGDPG (IN REF. 1).
FT A -> S (IN REF. 1).
FT QRQR -> HARG (IN REF. 1).
FT
SEQUENCE 122 AA; 13586 MW; 10783AB4896CF103 CRC64;

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Query Match      44.0%; Score 66; DB 1; Length 122;
Best Local Similarity 45.0%; Pred. No. 0.0044;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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RESULT 2
Q9UPH6 PRELIMINARY: PRT; 65 AA.
ID Q9UPH6
AC Q9UPH6
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE INL3_HUMAN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Scott D.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Sakalidis G., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Danganan L.,
RA Erler A., Christensen M., Georgescu A., Avila J., Attix C.,
RA Andreise T., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
RA Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Sanders C.,
RA Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;
RA "Sequence analysis of a 5.7 Mb region in 19p13.1.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007201; AAD22740.1; -
FT NON_TER 65
SQ SEQUENCE 65 AA; 7088 MW; 9D0BF767161DE030 CRC64;

Query Match 50.7%; Score 76; DB 4; Length 65;
Best Local Similarity 55.0%; Pred. No. 0.00026;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVITFCGSRW 27
Db 32 KLCGHHFVRALVRLCGPRW 51
:||||:||||:||||

RESULT 3
Q9NOT8 PRELIMINARY: PRT; 131 AA.
ID Q9NOT8
AC Q9NOT8
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RELAXIN-LIKE PROTEIN.
OS Dama dama (Fallow deer) (Cervus dama).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoides;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=30532;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20150568; PubMed=10687860;
RA Hombach-Klonisch S., Kauffold J., Rautenberg T., Steger K., Tetens F.,
RA Fischer B., Klonisch I.;
RA "Relaxin-like factor (RLF) mRNA expression in the fallow deer.";
RL Mol. Cell. Endocrinol. 159:147-158(2000).
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR EMBL; AF254740; AAF67742.1; -
DR EMBL; AF254740; AAF67742.1; -
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR SMART; SM00078; IIGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
SQ SEQUENCE 131 AA; 14406 MW; EC7731679E60B0C7 CRC64;

Query Match 50.0%; Score 75; DB 6; Length 131;
Best Local Similarity 55.0%; Pred. No. 0.00075;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVITFCGSRW 27
Db 32 KLCGHHFVRALVRLCGPRW 51
:||||:||||:||||

RESULT 4
Q9GK47 PRELIMINARY: PRT; 131 AA.
ID Q9GK47
AC Q9GK47
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RELAXIN-LIKE PROTEIN.
OS Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.
OX NCBI_TaxID=9463;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=TESTIS;
RA Klonisch T., Froehlich C., Tetens F., Fischer B., Hombach-Klonisch S.;
RA "Molecular remodeling of members of the relaxin family during primate
RA evolution.";
RL Mol. Biol. Evol. 0:0-0(2001).
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR EMBL; AF317624; AAG42317.1; -
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR SMART; SM00078; IIGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
SQ SEQUENCE 131 AA; 14414 MW; F18AFA9ACFC85943 CRC64;

Query Match 50.0%; Score 75; DB 6; Length 131;
Best Local Similarity 55.0%; Pred. No. 0.00075;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVITFCGSRW 27
Db 32 KLCGHHFVRALVRLCGPRW 51
:||||:||||:||||

RESULT 5
Q28431 PRELIMINARY: PRT; 33 AA.
ID Q28431
AC Q28431
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RELAXIN (FRAGMENT).
GN RLX.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA Evans B.B.A., Fu P., Tregear G.G.W.;
RA "Characterisation of primate relaxin genes.";
RL J. Mol. Endocrinol. 0:0-0(1993).
DR EMBL; Z27237; CAA81751.1; -
DR HSSP; P04090; 6RLX.
FT NON_TER 1
SQ SEQUENCE 33 AA; 3766 MW; 54BE68D028EDA2F6 CRC64;

Query Match 47.3%; Score 71; DB 6; Length 33;
Best Local Similarity 57.1%; Pred. No. 0.00073;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVITFCGSRW 27
Db 8 IKLCGRELVRQAICGMSTW 28
:||||:||||:||||

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Query Match      42.0%; Score 63; DB 6; Length 33;
Best Local Similarity 52.4%; Pred. No. 0.012;
Matches 11; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
    :||| | :|| | ||| |
Db 8 IKLCGCELVRAQIAICGMSTW 28

RESULT 8
Q9N0F2 PRELIMINARY; PRT; 73 AA.
AC Q9N0F2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE LEYDIG CELL-SPECIFIC INSULIN-LIKE PEPTIDE (FRAGMENT).
GN INSL3.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=THOROUGHbred; TISSUE=TESTIS;
RA Hasegawa T.;
RT "Nucleotide sequence of equine Leydig cell-specific insulin-like
    peptide."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB033169; BAA97580.1; -.
FT NON_TER 1
FT NON_TER 73
SQ SEQUENCE 73 AA; 8125 MW; B9DCBA6D0D72C8BD CRC64;

Query Match      40.7%; Score 61; DB 6; Length 73;
Best Local Similarity 52.9%; Pred. No. 0.056;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 11 GREFTIRAVFTCGGSRW 27
    | :||| : ||| |
Db 1 GHHFVRLVRCGGPRW 17

RESULT 9
Q9MYK8 PRELIMINARY; PRT; 180 AA.
AC Q9MYK8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RELAXIN.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99115216; PubMed=9915995;
RA Klonisch T., Hombach-Klonisch S., Froehlich C., Kauffold J.,
    Steger K., Huppertz B., Fischer B.;
RT "Nucleic acid sequence of feline preprorelaxin and its localization
    within the feline placenta";
RL Biol. Reprod. 60:305-311(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Hombach-Klonisch S., Klonisch T.;
    Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR EMBL; AF233688; AAF60303.1; -.
DR HSP; P04090; 6RLX.
DR InterPro; IPR000739; Insulin_IGF_relaxin.

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DR SMART: SM00078; ILGF: 1.
 DR PROSITE: PS00262; INSULIN: 1.
 SQ SEQUENCE 180 AA; 20360 MW; 4C2CF371C698AF9F CRC64;

Query Match 40.7%; Score 61; DB 6; Length 180;
 Best Local Similarity 47.6%; Pred. No. 0.14;
 Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 7 VRLCGREFIRAVIFTCGGSRW 27
 :: ||||| : || |
 Db 30 LKACGREFVRLQIRICGSLSW 50

RESULT 10
 Q28788 PRELIMINARY; PRT; 33 AA.

AC Q28788;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RELAXIN (FRAGMENT).
 GN RLX.
 OS Papio hamadryas (Hamadryas baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 OX NCBI_TaxID=9557;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BABA;
 RA Evans B.B.A., Fu P., Tregear G.G.W.;
 RT "Characterization of two relaxin genes in the chimpanzee."
 RL J. Mol. Endocrinol. 140:385-392(1994).
 DR EMBL; 227224; CAA81738.1; -.
 DR HSSP; P04090; 6RLX.
 FT NON_TER 1
 SQ SEQUENCE 33 AA; 3618 MW; DD8498A0353F9281 CRC64;

Query Match 38.0%; Score 57; DB 6; Length 33;
 Best Local Similarity 52.6%; Pred. No. 0.1;
 Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 7 VRLCGREFIRAVIFTCGGS 25
 :: ||||| : || |
 Db 8 IKACGRELVRQAICGKS 26

RESULT 11
 Q9NOT9 PRELIMINARY; PRT; 199 AA.

AC Q9NOT9;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PREPRORELAXIN.
 OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20191540; PubMed=10727251;
 RA Hombach-Klonisch S., Abd-Elmalek M., Skidmore J.A., Leiser R.,
 RA Fischer B., Klonisch T.;
 RT "Ruminant relaxin in the pregnant one-humped camel."
 RL Biol. Reprod. 62:839-846(2000).
 CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 DR EMBL; AF254739; AAF67741.1; -.
 DR HSSP; P01348; 1RLX.
 DR InterPro; IPR000739; Insulin_IGF_relaxin.

DR SMART: SM00078; ILGF: 1.
 DR PROSITE: PS00262; INSULIN: 1.
 SQ SEQUENCE 199 AA; 22386 MW; F69BBD7E4F4A8089 CRC64;

Query Match 38.0%; Score 57; DB 6; Length 199;
 Best Local Similarity 47.6%; Pred. No. 0.65;
 Matches 10; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 7 VRLCGREFIRAVIFTCGGSRW 27
 :: ||||| : || |
 Db 32 VRACGRELVRWLWIEICGSVSW 52

RESULT 12
 Q9TRG5 PRELIMINARY; PRT; 29 AA.

AC Q9TRG5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RELAXIN R-III B CHAIN.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93257096; PubMed=8489740;
 RA Kohsaka T., Takahara H., Sugawara K., Tagami S.;
 RT "Endogenous heterogeneity of relaxin and sequence of the major form in pregnant sow ovaries."
 RL Biol. Chem. Hoppe-Seyler 374:203-210(1993).
 DR HSSP; P01348; 1RLX.
 SQ SEQUENCE 29 AA; 3293 MW; 661A9F5DDDESDB10 CRC64;

Query Match 36.7%; Score 55; DB 6; Length 29;
 Best Local Similarity 38.1%; Pred. No. 0.18;
 Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 7 VRLCGREFIRAVIFTCGGSRW 27
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 Db 7 IKACGRELVRWLWIEICGSVSW 27

RESULT 13
 Q28782 PRELIMINARY; PRT; 33 AA.

AC Q28782;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RELAXIN (FRAGMENT).
 GN RLX.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DO PA;
 RA Evans B.B.A., Fu P., Tregear G.G.W.;
 RT "Characterisation of primate relaxin genes."
 RL J. Mol. Endocrinol. 0:0-0(1993).
 DR EMBL; 227230; CAA81744.1; -.
 DR HSSP; P04090; 6RLX.
 FT NON_TER 1
 SQ SEQUENCE 33 AA; 3752 MW; 225468D127FE9292 CRC64;

Query Match 36.0%; Score 54; DB 6; Length 33;
 Best Local Similarity 47.4%; Pred. No. 0.29;

us-09-781-077-2_copy_26_52.rspt

Fri Jun 28 11:32:07 2002